

WEST Search History

DATE: Monday, April 09, 2007

Hide?	Set Name	Query	Hit Count
		<i>DB=USPT; THES=ASSIGNEE; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L2	atcc adj5 209265.clm.	1
<input type="checkbox"/>	L1	atcc adj5 209265	29

END OF SEARCH HISTORY

Query Match	29.7%;	Score 477;	DB 1;	Length 310;
Best Local Similarity	37.0%;	Pred. NO. 7.4e-31;		
RESULT 8				
ID JAM3 HUMAN STANDARD;	PRT;	310 AA.		
DE Junctional adhesion molecule C precursor (JAM-C) (Junctional adhesion				
DE molecule 3) (JAM-3) (JAM-2).				
FT DISULFID 53 115		Potential.		
FT DISULFID 160 219		Potential.		
Query Match	28.8%;	Score 461.5;	DB 1;	Length 310;
Best Local Similarity	37.1%;	Pred. NO. 1.4e-29;		
RESULT 9				
ID Q66J15_XENTR PRELIMINARY;	PRT;	291 AA.		
DE MGC79514 protein.				
Query Match	27.7%;	Score 445;	DB 2;	Length 291;
Best Local Similarity	35.0%;	Pred. NO. 3e-28;		
RESULT 10				
ID Q2VPP6_XENLA PRELIMINARY;	PRT;	291 AA.		
DE Hypothetical protein.				
Query Match	27.4%;	Score 439.5;	DB 2;	Length 291;
Best Local Similarity	35.4%;	Pred. NO. 8.6e-28;		
RESULT 11				
ID Q640C0_XENLA PRELIMINARY;	PRT;	296 AA.		
DE LOC398527 protein (Fragment).				
Query Match	27.4%;	Score 439.5;	DB 2;	Length 296;
Best Local Similarity	35.4%;	Pred. NO. 8.8e-28;		
RESULT 12				
ID Q7SYQ7_XENLA PRELIMINARY;	PRT;	300 AA.		
DE LOC398527 protein (Fragment).				
Query Match	27.4%;	Score 439.5;	DB 2;	Length 300;
Best Local Similarity	35.4%;	Pred. NO. 9e-28;		
RESULT 13				
ID JAM1 FELCA STANDARD;	PRT;	298 AA.		
DE Junctional adhesion molecule A precursor (JAM-A) (Junctional adhesion				
DE molecule 1) (JAM-1) (CD321 antigen).				
FT DISULFID 49 108		By similarity.		
FT DISULFID 152 211		By similarity.		
Query Match	26.9%;	Score 431;	DB 1;	Length 298;
Best Local Similarity	36.0%;	Pred. NO. 4.5e-27;		
RESULT 14				
ID Q7ZWT0_XENLA PRELIMINARY;	PRT;	289 AA.		
DE MGC33721 protein.				
Query Match	26.1%;	Score 419.5;	DB 2;	Length 289;
Best Local Similarity	35.9%;	Pred. NO. 3.9e-26;		
RESULT 15				
ID Q4S0M3_TETNG PRELIMINARY;	PRT;	257 AA.		
DE Chromosome 2 SCAP14781 whole genome shotgun sequence.				
Query Match	25.8%;	Score 414;	DB 2;	Length 257;
Best Local Similarity	36.8%;	Pred. NO. 9.5e-26;		

OM protein - protein search, using sw model

Run on: April 10, 2007, 16:32:55 ; Search time 42 Seconds

(without alignments)

714.753 Million cell updates/sec

Title: US-10-785-221A-9

Perfect score: 1605

Sequence: 1 MARRSRHRLLLLLRYLVA.....TPVIPALWKAAGSGRGQFP 312

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	ID	Description
265	113.5	7.1	392	1	RWHUPD
266	113.5	7.1	417	1	RWHUPA

RESULT 1

A;Title: Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes redistribution of platelet activation by a stimulatory antibody: cross-linking of a

Query Match 25.2%; Score 404; DB 2; Length 299;

Best Local Similarity 35.2%; Pred. No. 1.9e-24;

RESULT 2

A;Title: Characterization of a cDNA encoding the bovine coxsackie and adenovirus receptor

Query Match 12.9%; Score 206.5; DB 2; Length 365;

Best Local Similarity 24.3%; Pred. No. 9.3e-09;

RESULT 3

A;Title: Genetic analysis of growth cone guidance in Drosophila: fasciclin II functions

Query Match 11.5%; Score 184; DB 2; Length 811;

Best Local Similarity 27.2%; Pred. No. 1.5e-06;

RESULT 4

A;Title: Genetic analysis of growth cone guidance in Drosophila: fasciclin II functions

Query Match 11.5%; Score 184; DB 2; Length 873;

Best Local Similarity 27.2%; Pred. No. 1.6e-06;

RESULT 5

Query Match 11.0%; Score 177; DB 2; Length 6642;

Best Local Similarity 28.6%; Pred. No. 6.7e-05;

RESULT 6

A;Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.

Query Match 10.8%; Score 169.5; DB 2; Length 7962;

Best Local Similarity 28.6%; Pred. No. 0.00032;

RESULT 7

A;Title: Molecular cloning of ssd-form neural cell adhesion molecules (N-CAMs) as the ma

Query Match 10.1%; Score 162; DB 2; Length 725;

Best Local Similarity 27.1%; Pred. No. 7e-05;

RESULT 8

A;Title: A receptor tyrosine kinase cDNA isolated from a population of enriched primitive

A;Title: High affinity VEGF binding and developmental expression suggest Flk-1 as a major

A;Title: NVK/FLK-1: a putative receptor protein tyrosine kinase isolated from E10 embryo

Query Match 10.1%; Score 162; DB 2; Length 1367;

Best Local Similarity 24.7%; Pred. No. 0.00015;

RESULT 9

A;Title: Molecular cloning of a gene for a member of carcinoembryonic antigen (CEA) gene

A;Title: Molecular cloning of a gene belonging to the carcinoembryonic antigen gene fami

A;Title: Primary structure of nonspecific crossreacting antigen (NCA), a member of carc

A;Title: Carcinoembryonic antigen family: characterization of cDNAs coding for NCA and C

A;Title: Characterization of a cDNA clone for the nonspecific cross-reacting antigen (NC

A;Title: Protein analysis of NCA-50 shows identity to NCA cDNA deduced sequences and ind

A;Title: Sequence and glycosylation site identity of two distinct glycoforms of nonspeci

A;Title: Sequence analysis of carcinoembryonic antigen: identification of glycosylation

A;Title: Identification of three new genes and estimation of the size of the carcinoemb

Query Match 10.0%; Score 161; DB 2; Length 344;

Best Local Similarity 26.5%; Pred. No. 3.4e-05;

RESULT 10

A;Title: Two neural-cell adhesion molecule(NCAM)-encoding genes in Xenopus laevis are ex

Query Match 9.8%; Score 158; DB 1; Length 1092;

Best Local Similarity 26.6%; Pred. No. 0.00024;

RESULT 11

A;Title: A novel brain-derived member of the epidermal growth factor family that interac

Query Match 9.8%; Score 157; DB 2; Length 860;

Best Local Similarity 27.7%; Pred. No. 0.00021;

RESULT 12

A;Title: A novel brain-derived member of the epidermal growth factor family that interac

Query Match 9.8%; Score 157; DB 2; Length 868;

Best Local Similarity 27.7%; Pred. No. 0.00021;

RESULT 13

A;Title: A new member of the immunoglobulin superfamily that has a cytoplasmic region ho

Query Match 9.7%; Score 156; DB 1; Length 1897;

Best Local Similarity 25.8%; Pred. No. 0.00066;

RESULT 14

Query Match 9.7%; Score 155.5; DB 2; Length 1328;

Best Local Similarity 27.5%; Pred. No. 0.00047;

RESULT 15

Query Match 9.7%; Score 155.5; DB 2; Length 2783;

Best Local Similarity 30.4%; Pred. No. 0.0012;

GenCore version 6.2
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OM protein - protein search, using sw model

Run on: April 10, 2007, 16:33:59 ; Search time 349 Seconds
(without alignments)
958.461 Million cell updates/sec

Title: US-10-785-221A-9

Perfect score: 1605

Sequence: 1 MARRSRHRLLLRLRYLVA.....TPVIPALMKAAAGSRGQGF 312

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : UniProt_8.4.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1475	91.9	298	1	JAM2_HUMAN
2	1184	73.8	298	1	Q3MHC0_RAT
3	1172	73.0	298	1	JAM2_MOUSE
4	598.5	37.3	243	2	Q5ZJDI_CHICK
5	517.5	32.2	181	2	Q9CWD9_MOUSE
6	479	29.8	310	1	JAM3_MOUSE
7	477	29.7	310	1	JAM3_RAT
8	461.5	28.8	310	1	JAM3_HUMAN
9	445	27.7	291	2	Q6GJ15_XENTR
10	439.5	27.4	291	2	Q2VPP6_XENLA
11	439.5	27.4	296	2	Q640C0_XENLA
12	439.5	27.4	300	2	Q7SYQ7_XENLA
13	431	26.9	298	1	JAM1_FELCA
14	419.5	26.1	289	2	Q7ZWT0_XENLA
15	414	25.8	257	2	Q4SOM3_TETNG
16	413	25.7	299	1	JAM1_HUMAN
17	404	25.2	299	1	Q6TIB4_HUMAN
18	404	25.2	299	1	JAM1_BOVIN
19	402.5	25.1	298	2	Q5E9V8_BOVIN
20	402.5	25.1	298	2	Q5E9V8_BOVIN
21	401.5	25.0	292	2	Q66172_BRARE
22	396.5	24.7	260	2	Q4S8Z8_TETNG
23	394	24.5	300	1	JAM1_MOUSE
24	394	24.5	300	2	Q8VC39_MOUSE
25	382	23.8	300	1	JAM1_RAT
26	379.5	23.6	273	2	Q4RRS6_TETNG
27	366.5	22.8	259	2	Q9Y5B2_HUMAN
28	284.5	17.7	173	2	Q9JXK5_RAT
29	238.5	14.9	319	2	Q3ZCC6_BOVIN
30	238	14.8	319	1	GRA33_HUMAN
31	238	14.8	319	2	Q5VZP6_HUMAN

32	229	14.3	335	2	Q9PWR4_CHICK	Q9PWR4 gallus gall
33	228	14.2	318	2	Q91664_XENLA	Q91664 xenopus lae
34	228	14.2	335	2	Q9YGH1_CHICK	Q9YGH1 gallus gall
35	226	14.1	319	1	QPA33_MOUSE	Q9JKA5 mus musculus
36	225.5	14.0	347	2	Q5XG4_XENTR	Q5XG4 xenopus tro
37	225.5	14.0	366	2	Q28D52_XENTR	Q28D52 xenopus tro
38	225.5	14.0	394	1	ESAM_RAT	Q6ayd4 rattus norv
39	217	13.5	181	2	Q91665_XENLA	Q91665 xenopus lae
40	214	13.3	335	2	Q9YGV5_CHICK	Q9YGV5 gallus gall
41	211.5	13.2	387	2	Q86XK7_HUMAN	Q86XK7 homo sapien
42	211.5	13.2	412	2	Q6MZS4_HUMAN	Q6mzs4 homo sapien
43	210	13.1	390	1	ESAM_HUMAN	Q56ap7 homo sapien
44	210	13.1	428	2	Q5U2F2_RAT	Q5U2F2 rattus norv
45	208.5	13.0	319	2	Q9TU80_CANFA	Q9TU80 canis faml
46	208.5	13.0	382	2	Q29RR6_BOVIN	Q29RR6 bos taurus
47	207.5	12.9	394	1	ESAM_MOUSE	Q925f2 mus musculus
48	207.5	12.9	394	2	Q3U1Q2_MOUSE	Q3U1Q2 mus musculus
49	207	12.9	442	2	Q6NW88_BRARE	Q6nw88 brachydanio
50	206.5	12.9	365	1	Q3XAR_BOVIN	Q8wmv3 bos taurus
51	206.5	12.9	365	2	Q3SZH9_BOVIN	Q3szh9 bos taurus
52	203.5	12.7	344	2	Q568F7_BRARE	Q568f7 brachydanio
53	203.5	12.6	332	2	Q6P359_XENTR	Q6p359 xenopus tro
54	198.5	12.4	365	1	Q3XAR_HUMAN	P78310 homo sapien
55	198.5	12.4	365	1	Q3XAR_PONPY	Q57f64 pongo pygma
56	198	12.3	407	2	Q9D2J4_MOUSE	Q9D2J4 mus musculus
57	196	12.2	319	2	Q9TU79_PIG	Q9TU79 sus scrofa
58	195.5	12.2	283	2	Q4V7Q4_XENLA	Q4V7Q4 xenopus lae
59	195	12.1	404	2	Q4KLY3_RAT	Q4KLY3 rattus norv
60	194.5	12.1	431	2	Q5DX21_HUMAN	Q5dx21 homo sapien
61	194	12.1	335	2	Q58E82_XENLA	Q58e82 xenopus lae
62	194	12.1	372	1	Q3XAR_BRARE	Q90y50 brachydanio
63	193	12.0	390	1	ESAM_MACFA	Q95ki3 macaca fasc
64	189.5	11.8	430	2	Q8N4F1_HUMAN	Q8n4f1 homo sapien
65	189.5	11.8	452	2	Q4RR70_TETNG	Q4rrt0 tetraodon n
66	186.5	11.6	210	2	Q4R7W7_MACFA	Q4R7W7 macaca fasc
67	185	11.5	365	1	Q6XAR_MOUSE	P97792 mus musculus
68	184	11.5	773	2	Q6IDE4_DROME	Q6ide4 drosophila
69	184	11.5	873	1	PAS2_DROME	P34082 drosophila
70	183	11.4	300	2	Q9DA22_MOUSE	Q9da22 mus musculus
71	183	11.4	300	2	Q9D9J0_MOUSE	Q9d9j0 mus musculus
72	182	11.3	365	1	Q3XAR_RAT	Q9R066 rattus norv
73	182	11.3	5533	2	Q5RIP6_BRARE	Q5rip6 brachydanio
74	179.5	11.2	417	2	Q5R6B7_PONPY	Q5r6b7 pongo pygma
75	179	11.2	323	2	Q8NDD2_HUMAN	Q8ndd2 homo sapien
76	179	11.2	432	2	Q6DDE7_XENLA	Q6dde7 xenopus lae
77	179	11.2	858	2	Q18466_HIRME	Q18466 hirudo medi
78	178	11.1	327	1	VSIG2_HUMAN	Q961q7 homo sapien
79	178	11.1	3950	2	Q7YRF5_CANFA	Q7yrf5 canis faml
80	177.5	11.1	328	1	VSIG2_MOUSE	Q92109 mus musculus
81	177.5	11.1	395	2	Q8BXJ7_MOUSE	Q8bxj7 mus musculus
82	177.5	11.1	395	2	Q8B2P4_MOUSE	Q8b2p4 mus musculus
83	177.5	11.1	395	2	Q1WIM2_RAT	Q1wim2 rattus norv
84	177.5	11.1	404	2	Q8BLQ9_MOUSE	Q8blq9 mus musculus
85	177	11.0	332	2	Q640U3_XENTR	Q640u3 xenopus tro
86	177	11.0	8081	1	UNC89_CAEEL	Q01761 caenorhabdi
87	176.5	11.0	417	2	Q2TBL2_BOVIN	Q2tbl2 bos taurus
88	176.5	11.0	848	2	Q7QC00_ANOGA	Q7qcu0 anopheles g
89	175.5	10.9	396	2	Q2KJAY_BOVIN	Q2kjay bos taurus
90	174.5	10.9	404	2	Q3KQY9_HUMAN	Q3kqy9 homo sapien
91	174.5	10.9	417	2	Q7TNL1_MOUSE	Q7tnl1 mus musculus
92	174	10.8	3493	2	Q4RJ20_TETNG	Q4rj20 tetraodon n
93	173.5	10.8	404	2	Q8BYP1_MOUSE	Q8byp1 mus musculus
94	173	10.8	352	2	Q3TV22_MOUSE	Q3tv22 mus musculus
95	171	10.7	322	2	Q4SHQ7_TETNG	Q4shq7 tetraodon n
96	171	10.7	5635	1	HMCN1_HUMAN	Q96rw7 homo sapien
97	169.5	10.6	34350	1	TITIN_HUMAN	Q8wz42 homo sapien
98	169	10.5	428	2	Q6F3J3_MOUSE	Q6f3j3 mus musculus
99	169	10.5	443	2	Q8N2F4_HUMAN	Q8n2f4 homo sapien
100	168.5	10.5	329	2	Q8N225_HUMAN	Q8n225 homo sapien
101	168.5	10.5	1340	2	Q8NDA2_HUMAN	Q8nda2 homo sapien
102	168	10.5	344	1	CEAM6_HUMAN	P40199 homo sapien
103	168	10.5	344	2	Q53XP7_HUMAN	Q53xp7 homo sapien
104	167.5	10.4	2672	2	Q3UHH3_MOUSE	Q3uhh3 m 14 days p

105	167	10.4	428	2	Q1WIL9 RAT	Q1wil9 rattus norv	178	156.5	9.8	1378	1	ROBO2_HUMAN	Q9hck4 homo sapien
106	167	10.4	582	2	Q8OWN2 MOUSE	Q8own2 mus musculus	179	156.5	9.8	1378	2	Q19AB4_HUMAN	Q19ab4 homo sapien
107	167	10.4	595	2	Q68SN8 MOUSE	Q68sn8 mus musculus	180	156.5	9.8	1394	2	Q19AB5_HUMAN	Q19ab5 homo sapien
108	166.5	10.4	442	2	Q9BY67 HUMAN	Q9by67 homo sapien	181	156	9.7	276	2	Q640S5_XENTR	Q640s5 xenopus tro
109	166	10.3	795	2	Q9OYM0 BRARE	Q9ym0 brachydanio	182	156	9.7	347	2	Q6PJ52_HUMAN	Q6pj52 homo sapien
110	165.5	10.3	735	2	Q4RZE9 TETNG	Q4rze9 tetraodon n	183	156	9.7	377	2	Q9VQY0_DROME	Q9vqy0 drosophila
111	165	10.3	405	2	Q6PFK4 BRARE	Q6pfk4 brachydanio	184	156	9.7	749	2	Q967D9_DROME	Q967d9 drosophila
112	164.5	10.2	414	2	Q5VU13 HUMAN	Q5vu13 homo sapien	185	156	9.7	756	1	NRG2_MOUSE	P56974 mus musculus
113	164.5	10.2	1038	2	Q4TK38 TETNG	Q4tk38 tetraodon n	186	156	9.7	902	2	Q81Q17_DROME	Q81q17 drosophila
114	164	10.2	401	2	Q3VIM4 MOUSE	Q3vim4 mus musculus	187	156	9.7	903	2	Q967D8_DROME	Q967d8 drosophila
115	164	10.2	837	1	NCAM2_MOUSE	Q35136 mus musculus	188	156	9.7	903	2	Q9VQY1_DROME	Q9vqy1 drosophila
116	163.5	10.2	373	2	Q9H6B4 HUMAN	Q9h6b4 homo sapien	189	156	9.7	1187	2	Q589G5_CHICK	Q589g5 gallus gall
117	163.5	10.2	846	2	Q57577 CYNPY	Q57577 cynops pyrr	190	156	9.7	1343	1	VGRF2_FAT	Q08775 rattus norv
118	163	10.2	1100	2	Q57576 CYNPY	Q57576 cynops pyrr	191	156	9.7	1484	2	Q5W9G3_HUMAN	Q5w9g3 homo sapien
119	163	10.2	433	2	Q6DJ83_XENTR	Q6dj83 xenopus tro	192	156	9.7	1508	2	Q6NR34_DROME	Q6nr34 drosophila
120	163	10.2	875	2	Q4RRR9 TETNG	Q4rrr9 tetraodon n	193	156	9.7	1508	2	Q9VQY2_DROME	Q9vqy2 drosophila
121	163	10.2	1431	2	Q8U060 MOUSE	Q8u060 mus musculus	194	156	9.7	1331	2	Q967D7_DROME	Q967d7 drosophila
122	162	10.1	237	2	Q6DQX5 RABIT	Q6dqx5 oryctolagus	195	156	9.7	1897	1	PTPRF_HUMAN	P10586 homo sapien
123	162.5	10.1	952	2	Q4SPY1 TETNG	Q4spy1 tetraodon n	196	156	9.7	1898	2	Q5T021_HUMAN	Q5t021 homo sapien
124	162	10.1	725	2	Q73634_XENLA	Q73634 xenopus lae	197	156	9.7	1898	2	Q86WS0_HUMAN	Q86ws0 homo sapien
125	162	10.1	1345	2	Q8VCD0 MOUSE	Q8vcd0 mus musculus	198	156	9.7	1903	2	Q5SPJ6_MOUSE	Q5spj6 mus musculus
126	162	10.1	1367	1	VGRF2_MOUSE	Q35918 mus musculus	199	156	9.7	1907	2	Q5T022_HUMAN	Q5t022 homo sapien
127	162	10.1	4071	2	Q6KDZ1_CHICK	Q6kdz1 gallus gall	200	156	9.7	1318	2	Q5W9G2_HUMAN	Q5w9g2 homo sapien
128	161.5	10.1	445	2	Q8R4L1 MOUSE	Q8r4l1 mus musculus	201	155.5	9.7	481	2	Q5K373_BRARE	Q5k373 brachydanio
129	161.5	10.1	445	2	Q8K3T6 MOUSE	Q8k3t6 mus musculus	202	155.5	9.7	481	2	Q5K374_BRARE	Q5k374 brachydanio
130	161.5	10.1	723	2	Q29FP8_DROPS	Q29fp8 drosophila	203	155.5	9.7	722	2	Q4KMG2_HUMAN	Q4kmg2 homo sapien
131	161.5	10.1	979	2	Q4TBU1_TETNG	Q4tbu1 tetraodon n	204	155.5	9.7	1328	2	Q21043_CABEL	Q21043 caenorhabdi
132	161	10.0	344	2	Q13774_HUMAN	Q13774 homo sapien	205	155.5	9.7	1460	2	Q5HZ61_XENTR	Q5hz61 xenopus tro
133	161	10.0	456	2	Q8R5M8 MOUSE	Q8r5m8 mus musculus	206	155.5	9.7	1496	2	Q92626_HUMAN	Q92626 homo sapien
134	161	10.0	727	2	Q6RKB2 RAT	Q6rkb2 rattus norv	207	155	9.7	299	2	Q3MI86_HUMAN	Q3mi86 homo sapien
135	161	10.0	837	2	Q6RKB3 RAT	Q6rkb3 rattus norv	208	155	9.7	476	2	Q6APY5_RAT	Q6apy5 rattus norv
136	161	10.0	1694	2	Q17F85_AEDAE	Q17f85 aedes aegypt	209	155	9.7	521	1	CEAM1_MOUSE	Q66iv0 xenopus lae
137	160.5	10.0	1049	2	Q4RVM2_TETNG	Q4rvm2 tetraodon n	210	155	9.7	719	2	Q66IV0_XENLA	Q66iv0 xenopus lae
138	160.5	10.0	2693	2	Q8ISFP3_CABEL	Q8isf3 caenorhabdi	211	155	9.7	725	2	Q73633_XENLA	Q73633 xenopus lae
139	160.5	10.0	2708	2	Q8ISF4_CABEL	Q8isf4 caenorhabdi	212	155	9.7	850	1	NRG2_HUMAN	Q14511 homo sapien
140	160.5	10.0	18519	2	Q8ISF6_CABEL	Q8isf6 caenorhabdi	213	155	9.7	1088	1	NCA11_XENLA	P16170 xenopus lae
141	160.5	10.0	18534	2	Q8ISF7_CABEL	Q8isf7 caenorhabdi	214	155	9.7	1475	2	Q3UQ28_MOUSE	Q3uq28 mus musculus
142	160	10.0	837	1	NCAM2_HUMAN	Q15394 homo sapien	215	154.5	9.6	262	2	Q308M3_HUMAN	Q308m3 homo sapien
143	160	10.0	1209	2	Q7PG72_ANOGA	Q7pg72 anopheles g	216	154.5	9.6	368	2	Q5UB49_HUMAN	Q5ub49 homo sapien
144	160	10.0	1215	2	Q7QEC1_ANOGA	Q7qec1 anopheles g	217	154.5	9.6	388	2	Q8NPF28_HUMAN	Q8nfp28 brachydanio
145	160	10.0	1237	2	Q29FMI_DROPS	Q29fmi drosophila	218	154.5	9.6	1032	2	Q8UVD6_BRARE	Q8uvd6 brachydanio
146	160	10.0	1306	2	Q29LF7_DROPS	Q29lf7 drosophila	219	154.5	9.6	1323	2	Q08476_CHICK	Q08476 gallus gall
147	159.5	9.9	226	2	Q4RDM1_TETNG	Q4rdm1 tetraodon n	220	154.5	9.6	1421	2	Q16FY3_AEDAE	Q16fy3 aedes aegypt
148	159.5	9.9	545	2	Q7QDVI1_ANOGA	Q7qdv1 anopheles g	221	154.5	9.6	1450	2	Q4SCT9_TETNG	Q4sct9 tetraodon n
149	159.5	9.9	2528	2	Q4S2G3_TETNG	Q4s2g3 tetraodon n	222	154.5	9.6	4391	1	PGBM_HUMAN	P98160 homo sapien
150	159	9.9	803	2	Q80ZF5_RAT	Q80zf5 rattus norv	223	154.5	9.6	4391	2	Q5VU27_HUMAN	Q5vu27 homo sapien
151	159	9.9	837	2	Q727F2_HUMAN	Q727f2 homo sapien	224	154	9.6	521	2	Q925P3_MOUSE	Q925p3 mus musculus
152	158.5	9.9	319	2	Q7OLK4_ANOGA	Q7olk4 anopheles g	225	154	9.6	2009	2	Q695L3_BRARE	Q695l3 brachydanio
153	158.5	9.9	981	2	Q290N5_DROPS	Q290n5 drosophila	226	154	9.6	2597	2	Q6WRH9_RAT	Q6wrh9 rattus norv
154	158.5	9.9	1048	2	Q7OH02_ANOGA	Q7oh02 anopheles g	227	153.5	9.6	333	2	Q90Z41_CHICK	Q90z41 gallus gall
155	158	9.8	276	2	Q28GJ3_XENTR	Q28gj3 xenopus tro	228	153.5	9.6	368	2	Q6RWT3_BOVIN	Q6rwt3 bos taurus
156	158	9.8	291	2	Q658Q7_HUMAN	Q658q7 homo sapien	229	153.5	9.6	376	2	Q90Z71_BRARE	Q90z71 brachydanio
157	158	9.8	605	2	Q8TBU0_HUMAN	Q8tbu0 homo sapien	230	153.5	9.6	483	2	Q32LG4_BOVIN	Q32lg4 bos taurus
158	158	9.8	673	2	Q6MZW2_HUMAN	Q6mzw2 homo sapien	231	153.5	9.6	831	2	Q71SY9_CHICK	Q71sy9 gallus gall
159	158	9.8	693	2	Q9UPU1_HUMAN	Q9upu1 homo sapien	232	153.5	9.6	1001	2	Q5TR64_ANOGA	Q5tr64 anopheles g
160	158	9.8	1092	1	NCAL12_XENLA	Q36335 xenopus lae	233	153.5	9.6	1228	2	Q8MBA3_DROME	Q8mba3 drosophila
161	158	9.8	1343	2	Q5FQU0_RAT	Q5fqu0 rattus norv	234	153.5	9.6	1235	2	Q86BD5_DROME	Q86bd5 drosophila
162	157.5	9.8	81	2	Q3ODR8 SHEEP	Q3od8 ovis aries	235	153.5	9.6	1470	1	ROBO2_MOUSE	Q9v787 drosophila
163	157.5	9.8	302	2	Q4T3Z1_TETNG	Q4t3z1 tetraodon n	236	153.5	9.6	1505	2	Q7Q623_ANOGA	Q7q623 anopheles g
164	157.5	9.8	854	2	Q4ACB3_BRARE	Q4acb3 brachydanio	237	153.5	9.6	1508	2	Q19AB2_MOUSE	Q19ab2 mus musculus
165	157.5	9.8	1534	2	Q4RRJ4_TETNG	Q4rrj4 tetraodon n	238	153.5	9.6	1527	2	Q19AB3_MOUSE	Q19ab3 mus musculus
166	157	9.8	435	2	Q5FWW6_XENLA	Q5fww6 xenopus lae	239	153.5	9.6	1675	2	Q98SW4_BRARE	Q98sw4 brachydanio
167	157	9.8	868	1	NRG2_RAT	Q35569 rattus norv	240	153.5	9.6	231	2	Q50210_BRARE	Q50210 brachydanio
168	157	9.8	1342	2	Q9GPP6_DROME	Q9gpp6 drosophila	241	153	9.5	231	2	Q50210_BRARE	Q50210 brachydanio
169	157	9.8	1342	2	Q9VPE7_DROME	Q9vpe7 drosophila	242	153	9.5	241	2	Q4T426_TETNG	Q4t426 tetraodon n
170	157	9.8	1887	2	Q9W677_9MURI	Q9w677 rattus sp.	243	153	9.5	300	2	Q7PV30_ANOGA	Q7pv30 anopheles g
171	156.5	9.8	435	2	Q8N3J6_HUMAN	Q8n3j6 homo sapien	244	153	9.5	508	2	Q8BJA5_MOUSE	Q8bj5 mus musculus
172	156.5	9.8	437	2	Q81ZP8_HUMAN	Q81zp8 homo sapien	245	153	9.5	520	2	Q925P2_MOUSE	Q925p2 mus musculus
173	156.5	9.8	779	2	Q97136 MANSE	Q97136 manduca sex	246	153	9.5	847	1	FSTL5_HUMAN	Q8n475 homo sapien
174	156.5	9.8	814	2	Q16WM8_AEDAE	Q16wm8 aedes aegypt	247	153	9.5	882	2	Q4RVZ3_TETNG	Q4rvz3 tetraodon n
175	156.5	9.8	837	2	Q97137 MANSE	Q97137 manduca sex	248	153	9.5	1031	2	Q90YM2_BRARE	Q90ym2 brachydanio
176	156.5	9.8	893	2	Q5TNT4_ANOGA	Q5tnt4 anopheles g	249	153	9.5	4162	2	Q98918_CHICK	Q98918 gallus gall
177	156.5	9.8	1089	2	Q4S556_TETNG	Q4s556 tetraodon n	250	152.5	9.5	365	2	Q6VAN5_BOVIN	Q6van5 bos taurus

251	152.5	9.5	396	1	IGS4B_MOUSE	Q99n28	mus musculus	324	149	9.3	1501	2	Q7TT17_MOUSE	Q7tt17	mus musculus
252	152.5	9.5	396	2	Q1WIM3_RAT	Q1wim3	rattus norv	325	149	9.3	1904	2	Q64699_MOUSE	Q64699	mus musculus
253	152.5	9.5	458	2	Q17LIV3_AEDAE	Q17liv3	aedes aegyp	326	149	9.3	1907	2	Q4JFC7_MOUSE	Q4jfc7	mus musculus
254	152.5	9.5	690	2	Q5ISL0_MACFA	Q5isl0	macaca fasc	327	148.5	9.3	336	2	Q29NN8_DROPS	Q29nn8	drosophila
255	152.5	9.5	850	2	Q4S3Y6_TETNG	Q4s3y6	tetraodon n	328	148.5	9.3	436	2	Q6VAN8_BOVIN	Q6van8	bos taurus
256	152.5	9.5	1091	1	NCAM1_CHICK	Q13590	gallus gall	329	148.5	9.3	838	2	Q90YM1_BRARE	Q90ym1	brachydanio
257	152.5	9.5	1285	2	Q16RH0_AEDAE	Q16rh0	aedes aegyp	330	148.5	9.3	1242	2	Q1KMS5_BRARE	Q1kms5	brachydanio
258	152	9.5	696	2	Q5DU03_MOUSE	Q5du03	mus musculus	331	148.5	9.3	1253	2	Q4SCT8_TETNG	Q4sct8	tetraodon n
259	152	9.5	846	2	Q5RIQ0_FELCA	Q5riq0	felis silve	332	148.5	9.3	1496	2	Q3KPI9_HUMAN	Q3kpi9	homo sapien
260	152	9.5	847	2	Q5G7G8_FELCA	Q5g7g8	felis silve	333	148	9.2	359	1	LACH_DROME	Q24372	drosophila
261	152	9.5	1032	2	Q24327_DROME	Q24327	drosophila	334	148	9.2	428	2	Q290N6_DROPS	Q290n6	drosophila
262	152	9.5	1302	1	NRG_DROME	P20241	drosophila	335	148	9.2	839	2	Q8BQ96_MOUSE	Q8bq96	mus musculus
263	152	9.5	5175	2	Q8I0L3_CAEBL	Q8i0l3	caenorhabdi	336	148	9.2	839	2	Q8C4B2_MOUSE	Q8c4b2	mus musculus
264	152	9.5	5198	2	Q76518_CAEBL	Q76518	caenorhabdi	337	148	9.2	841	2	Q5STE3_MOUSE	Q5ste3	mus musculus
265	151.5	9.4	345	2	Q811H7_MOUSE	Q811h7	mus musculus	338	148	9.2	849	2	Q3T1H3_RAT	Q3t1h3	rattus norv
266	151.5	9.4	352	2	Q76697_CAEBL	Q76697	caenorhabdi	339	148	9.2	858	1	NCAM1_RAT	P13596	rattus norv
267	151.5	9.4	413	2	Q699P0_ANTPE	Q699p0	antheraea p	340	148	9.2	1070	2	Q4S2F2_TETNG	Q4s2f2	tetraodon n
268	151.5	9.4	521	2	Q61352_MOUSE	Q61352	mus musculus	341	148	9.2	1379	2	P79701_COTCO	P79701	coturnix co
269	151.5	9.4	761	1	NCA12_HUMAN	P13592	homo sapien	342	148	9.2	1513	2	Q90Z70_BRARE	Q90z70	brachydanio
270	151.5	9.4	807	2	Q59FL7_HUMAN	Q59fl7	homo sapien	343	147.5	9.2	275	2	Q8AVV1_XENLA	Q8avv1	xenopus lae
271	151.5	9.4	848	1	NCA11_HUMAN	P13591	homo sapien	344	147.5	9.2	333	1	AMAL_DROME	P15364	drosophila
272	151.5	9.4	848	2	Q25198_HYDAT	Q25198	hydra atten	345	147.5	9.2	341	2	Q7KSX2_DROME	Q7ksx2	drosophila
273	151.5	9.4	858	2	Q86X47_HUMAN	Q86x47	homo sapien	346	147.5	9.2	389	2	Q5U3R8_BRARE	Q5u3r8	brachydanio
274	151.5	9.4	1287	1	CDON_HUMAN	Q4kmg0	homo sapien	347	147.5	9.2	390	2	Q66KX2_XENLA	Q66kx2	xenopus lae
275	151.5	9.4	1301	2	Q4RSG5_TETNG	Q4rsg5	tetraodon n	348	147.5	9.2	484	2	Q17NY0_AEDAE	Q17ny0	aedes aegyp
276	151.5	9.4	1693	2	Q4S6A5_MOUSE	Q4s6a5	tetraodon n	349	147.5	9.2	943	2	Q7PRK4_ANOGA	Q7prk4	anopheles g
277	151	9.4	248	2	Q3TQ52_MOUSE	Q3tq52	mus musculus	350	147.5	9.2	1271	2	Q6U7I4_BRARE	Q6u7i4	brachydanio
278	151	9.4	375	2	Q6RWT4_BOVIN	Q6rwt4	bos taurus	351	147.5	9.2	1435	2	Q28V51_DROPS	Q28v51	drosophila
279	151	9.4	432	2	Q6RWT5_BOVIN	Q6rwt5	bos taurus	352	147.5	9.2	1505	2	Q3KPJ0_HUMAN	Q3kpj0	homo sapien
280	151	9.4	670	2	Q3TZW7_MOUSE	Q3tzw7	mus musculus	353	147.5	9.2	1506	2	Q3KPJ1_HOMEN	Q3kpj1	homo sapien
281	151	9.4	1702	2	Q4RJ21_TETNG	Q4rj21	tetraodon n	354	147.5	9.2	1912	1	PTPRD_HUMAN	P23468	homo sapien
282	151	9.4	1898	2	Q9EQ17_MOUSE	Q9eq17	mus musculus	355	147.5	9.2	1912	2	Q2HXI4_HUMAN	Q2hxi4	homo sapien
283	151	9.4	10495	2	Q4RE92_TETNG	Q4re92	tetraodon n	356	147.5	9.2	2057	2	Q4T2N4_TETNG	Q4t2n4	tetraodon n
284	150.5	9.4	296	2	Q42404_CHICK	Q42404	gallus gall	357	147	9.2	323	2	Q7QBA7_ANOGA	Q7qba7	anopheles g
285	150.5	9.4	388	2	Q1WIM1_RAT	Q1wim1	rattus norv	358	147	9.2	358	2	Q90490_BRARE	Q90490	brachydanio
286	150.5	9.4	791	2	Q16EG8_AEDAE	Q16eg8	aedes aegyp	359	147	9.2	406	2	Q8N7T8_HUMAN	Q8n7t8	homo sapien
287	150.5	9.4	1051	1	PTK7_CHICK	Q91048	gallus gall	360	147	9.2	454	2	Q91W54_MOUSE	Q91w54	mus musculus
288	150.5	9.4	1199	2	Q21041_CAEBL	Q21041	caenorhabdi	361	147	9.2	525	2	Q5R9N6_PONPY	Q5-9n6	pongo pygma
289	150.5	9.4	1239	2	Q28ZM3_DROPS	Q28zm3	drosophila	362	147	9.2	725	2	Q512D5_CANFA	Q512d5	canis famill
290	150.5	9.4	1345	2	Q174G3_AEDAE	Q174g3	aedes aegyp	363	147	9.2	847	2	Q512D7_CANFA	Q512d7	canis famill
291	150.5	9.4	1349	2	Q291P5_DROPS	Q291p5	drosophila	364	147	9.2	857	2	Q512D6_CANFA	Q512d6	canis famill
292	150	9.3	372	2	Q6VAN6_BOVIN	Q6van6	bos taurus	365	147	9.2	4129	2	Q59B65_DROME	Q59b65	drosophila
293	150	9.3	429	2	Q6VAN7_BOVIN	Q6van7	bos taurus	366	146.5	9.1	392	2	Q3UQW4_MOUSE	Q3uqw4	mus musculus
294	150	9.3	433	2	Q9V644_DROME	Q9v644	drosophila	367	146.5	9.1	409	2	Q4SFV2_TETNG	Q4sfv2	tetraodon n
295	150	9.3	847	1	FSTI15_MOUSE	Q8bfr2	mus musculus	368	146.5	9.1	508	1	FCRL2_HUMAN	Q961a5	homo sapien
296	150	9.3	847	2	Q3UUI4_MOUSE	Q3uui4	mus musculus	369	146.5	9.1	904	2	Q7PME2_ANOGA	Q7pme2	anopheles g
297	150	9.3	1250	1	CDON_MOUSE	Q32md9	mus musculus	370	146.5	9.1	1056	2	Q90Z03_XENLA	Q90z03	xenopus lae
298	150	9.3	1280	2	Q4RRJ3_TETNG	Q4rrj3	tetraodon n	371	146.5	9.1	1093	1	LRIG1_HUMAN	Q96faj	homo sapien
299	150	9.3	1501	2	Q4JFL8_RAT	Q4jfl8	rattus norv	372	146.5	9.1	1093	2	Q5XWD3_HUMAN	Q5xwd3	homo sapien
300	150	9.3	1501	2	Q9QW00_9MURI	Q9qw00	rattus norv	373	146.5	9.1	1505	2	Q3KPJ2_HUMAN	Q3kpj2	homo sapien
301	150	9.3	1863	2	Q64605_RAT	Q64605	rattus norv	374	146.5	9.1	1612	1	ROBO1_MOUSE	Q89026	mus musculus
302	150	9.3	1898	2	Q64604_RAT	Q64604	rattus norv	375	146.5	9.1	1651	1	ROBO1_RAT	Q55005	rattus norv
303	150	9.3	1907	2	Q3KRE9_RAT	Q3kre9	rattus norv	376	146	9.1	128	2	Q1LY86_BRARE	Q1ly86	brachydanio
304	149.5	9.3	89	2	Q4T2E5_TETNG	Q4te25	tetraodon n	377	146	9.1	353	2	Q86XY3_HUMAN	Q86xy3	homo sapien
305	149.5	9.3	349	1	CEAM8_HUMAN	P31997	homo sapien	378	146	9.1	373	2	Q7KVP5_HUMAN	Q7kvp5	homo sapien
306	149.5	9.3	372	2	Q8KLG0_RAT	Q8klg0	rattus norv	379	146	9.1	434	2	Q6DN72_HUMAN	Q6dn72	homo sapien
307	149.5	9.3	373	2	Q8R373_MOUSE	Q8r373	mus musculus	380	146	9.1	464	2	Q16170_HUMAN	Q16170	homo sapien
308	149.5	9.3	388	2	Q8R464_MOUSE	Q8r464	mus musculus	381	146	9.1	468	2	Q96CA7_HUMAN	Q96ca7	homo sapien
309	149.5	9.3	439	2	Q6RWT6_BOVIN	Q6rwt6	bos taurus	382	146	9.1	493	2	Q3KRG8_HUMAN	Q3krg8	homo sapien
310	149.5	9.3	519	1	CEAM1_RAT	P16573	rattus norv	383	146	9.1	526	1	CEAM1_HUMAN	P13688	homo sapien
311	149.5	9.3	1033	2	Q9V643_DROME	Q9v643	drosophila	384	146	9.1	605	2	Q921P2_MOUSE	Q921p2	mus musculus
312	149.5	9.3	1264	2	P91767_MANSE	P91767	manduca sex	385	146	9.1	1479	2	Q7KQT5_DROME	Q7kqt5	drosophila
313	149.5	9.3	1406	2	Q9GPP7_DROME	Q9gpp7	drosophila	386	146	9.1	1482	2	Q9V4Y0_DROME	Q9v4y0	drosophila
314	149.5	9.3	1463	2	Q9VQ08_DROME	Q9vq08	drosophila	387	146	9.1	1788	2	Q9IAJ0_XENLA	Q9iaj0	xenopus lae
315	149.5	9.3	1551	1	Q1RMC7_HUMAN	Q1rmc7	homo sapien	388	145.5	9.1	373	2	Q20S05_MOUSE	Q20s05	mus musculus
316	149.5	9.3	7968	1	OBSCN_HUMAN	Q5vct9	homo sapien	389	145.5	9.1	843	2	Q5EA96_BOVIN	Q5ea96	bos taurus
317	149	9.3	349	2	Q1POE3_DROMI	Q1pqe3	drosophila	390	145.5	9.1	1077	2	Q5WN88_CAEBR	Q5wn88	caenorhabdi
318	149	9.3	524	2	Q7PSU8_ANOGA	Q7psu8	anopheles g	391	145.5	9.1	1193	2	Q2VMP9_RAT	Q2vmp9	rattus norv
319	149	9.3	605	2	Q6GNL9_XENLA	Q6gnl9	xenopus lae	392	145.5	9.1	1340	2	Q5UI76_DROME	Q5ui76	drosophila
320	149	9.3	1277	1	L1CAM_FUGRU	Q98902	fugu rubrip	393	145.5	9.1	1607	2	Q1RMC8_HUMAN	Q1rmc8	homo sapien
321	149	9.3	1393	2	Q29LFI_DROPS	Q29lfi	drosophila	394	145.5	9.1	1607	2	Q2MIJ3_HUMAN	Q2mij3	homo sapien
322	149	9.3	1497	2	Q5XJV4_MOUSE	Q5xjv4	mus musculus	395	145.5	9.1	1651	1	ROBO1_HUMAN	Q9y6n7	homo sapien
323	149	9.3	1499	2	Q90815_CHICK	Q90815	gallus gall	396	145.5	9.1	1709	1	SN_HUMAN	Q9bz22	homo sapien

397	145	9.0	853	1	NCAM1_BOVIN	P31836 bos taurus	470	142	8.8	458	2	Q63093_RAT	Q63093 rattus norv
398	145	9.0	1028	2	Q6INB5_XENLA	Q6inb5 xenopus lae	471	142	8.8	532	2	Q6NNU3_DROME	Q6nnu3 drosophila
399	145	9.0	1244	2	Q69YJ3_HUMAN	Q69yj3 homo sapien	472	142	8.8	740	2	Q96P29_HUMAN	Q96p29 homo sapien
400	145	9.0	1357	2	Q5MD89_BRARE	Q5md89 brachydanio	473	142	8.8	847	1	CD22_HUMAN	P20273 homo sapien
401	145	9.0	1357	2	Q5GIT7_BRARE	Q5git2 brachydanio	474	142	8.8	854	2	Q17HA9_AEDAE	Q17ha9 aedes aegyp
402	145	9.0	1395	2	Q44924_DROME	Q44924 drosophila	475	142	8.8	1237	2	Q610C8_CAEBR	Q610c8 caenorhabdi
403	145	9.0	1395	2	Q7KWJ3_DROME	Q7kwj3 drosophila	476	142	8.8	1501	2	Q2M3R7_HUMAN	Q2m3r7 homo sapien
404	145	9.0	1429	2	Q9W213_DROME	Q9w213 drosophila	477	142	8.8	1560	2	Q59FX6_HUMAN	Q59fx6 homo sapien
405	145	9.0	1905	2	Q5VVL9_HUMAN	Q5vvl9 homo sapien	478	142	8.8	1730	2	Q7YRQ7_PIG	Q7yrg7 sus scrofa
406	145	9.0	2506	2	Q299Y6_DROPS	Q299y6 drosophila	479	142	8.8	1730	2	Q2VF24_PIG	Q2vff2 sus scrofa
407	144.5	9.0	316	2	Q8WP58_DROSI	Q8wp58 drosophila	480	141.5	8.8	293	2	Q3RPI0_HUMAN	Q3kpi0 homo sapien
408	144.5	9.0	316	2	Q8WP94_DROSI	Q8wp94 drosophila	481	141.5	8.8	312	2	Q66KV0_XENLA	Q66kv0 xenopus lae
409	144.5	9.0	316	2	Q8WP93_DROSI	Q8wp93 drosophila	482	141.5	8.8	344	1	NTRI_RAT	Q62718 rattus norv
410	144.5	9.0	381	2	Q2YHU6_CHICK	Q2yhu6 gallus gall	483	141.5	8.8	405	2	Q7PRJ5_ANOGA	Q7prj5 anopheles g
411	144.5	9.0	389	2	Q29F09_DROPS	Q29f09 drosophila	484	141.5	8.8	483	2	Q9DBP8_MOUSE	Q9dbp8 mus musculu
412	144.5	9.0	1048	2	Q7QH01_ANOGA	Q7qh01 anopheles g	485	141.5	8.8	508	2	Q8R007_MOUSE	Q8r007 mus musculu
413	144.5	9.0	1060	2	Q9QZ13_RAT	Q9qz13 rattus norv	486	141.5	8.8	509	2	Q9EQY5_MOUSE	Q9eqy5 m mman-g pr
414	144.5	9.0	1110	1	BOC_MOUSE	Q6azb0 mus musculu	487	141.5	8.8	572	2	Q3U318_MOUSE	Q3u318 mus musculu
415	144.5	9.0	1269	2	Q01632_CAEBL	Q01632 caenorhabdi	488	141.5	8.8	635	2	Q4S1S8_TETNG	Q4sls8 tetraodon n
416	144.5	9.0	1273	2	Q44928_CAEBL	Q44928 caenorhabdi	489	141.5	8.8	635	2	Q17BD5_AEDAE	Q17bd5 aedes aegyp
417	144.5	9.0	1285	2	Q5TYT1_BRARE	Q5tyt1 brachydanio	490	141.5	8.8	1355	2	Q2XPT7_CANFA	Q2xpt7 canis famil
418	144.5	9.0	1335	2	Q610C7_CAEBR	Q610c7 caenorhabdi	491	141.5	8.8	1355	2	Q7QGT8_ANOGA	Q7qgt8 anopheles g
419	144.5	9.0	3707	1	PGEM_MOUSE	Q05793 mus musculu	492	141	8.8	154	2	Q7PSN2_ANOGA	Q7psn2 anopheles g
420	144.5	9.0	4463	2	Q8MLD8_DROME	Q8mld8 drosophila	493	141	8.8	218	2	Q7PJ18_ANOGA	Q7pj18 anopheles g
421	144.5	9.0	9270	2	Q8MLD9_DROME	Q8mld9 drosophila	494	141	8.8	296	2	Q29890_HUMAN	Q29890 homo sapien
422	144	9.0	292	2	Q4RFQ9_TETNG	Q4rfq9 tetraodon n	495	141	8.8	333	2	Q86WB8_HUMAN	Q86wb8 homo sapien
423	144	9.0	384	2	Q1RKW0_DROME	Q1rkw0 drosophila	496	141	8.8	459	2	Q3TAA6_MOUSE	Q3taa6 mus musculu
424	144	9.0	403	2	Q9VP08_DROME	Q9vp08 drosophila	497	141	8.8	529	2	Q4SMH3_TETNG	Q4smh3 tetraodon n
425	144	9.0	662	2	Q60926_HUMAN	Q60926 homo sapien	498	141	8.8	532	2	Q9VLF0_DROME	Q9vlf0 drosophila
426	144	9.0	702	2	Q8N4D0_HUMAN	Q8n4d0 homo sapien	499	141	8.8	675	2	Q32M46_HUMAN	Q32m46 homo sapien
427	144	9.0	725	1	ICCR12_MOUSE	P13594 mus musculu	500	141	8.8	862	1	CD22_MOUSE	P33329 mus musculu
428	144	9.0	764	1	ICCR1_MOUSE	Q08180 drosophila	501	141	8.8	868	2	Q3TAX0_MOUSE	Q3tax0 mus musculu
429	144	9.0	862	2	Q4SAP3_TETNG	Q4sap3 tetraodon n	502	141	8.8	868	2	Q3UP36_MOUSE	Q3up36 mus musculu
430	144	9.0	1115	1	NCA11_MOUSE	P13595 mus musculu	503	141	8.8	868	2	Q3U0M3_MOUSE	Q3u0m3 mus musculu
431	144	9.0	1502	2	Q9UM81_HUMAN	Q9um81 homo sapien	504	141	8.8	932	2	Q3T9T5_MOUSE	Q3t9t5 mus musculu
432	144	9.0	1614	2	Q8UVD7_XENLA	Q8uvd7 xenopus lae	505	141	8.8	955	2	Q8MQ86_CAEBL	Q8mq86 caenorhabdi
433	144	9.0	1827	2	Q9VSG5_DROME	Q9vsg5 drosophila	506	141	8.8	1150	2	Q4SL82_TETNG	Q4sl82 tetraodon n
434	144	9.0	2331	2	Q59EG0_HUMAN	Q59eg0 homo sapien	507	141	8.8	1278	2	Q4RRS5_TETNG	Q4rrs5 tetraodon n
435	144	9.0	3198	2	Q9U8G8_MANSE	Q9u8g8 manduca sex	508	141	8.8	2016	2	Q9NBA1_DROME	Q9nba1 drosophila
436	143.5	8.9	398	1	IGS4B8_HUMAN	Q8n126 homo sapien	509	141	8.8	2051	2	Q44328_HIRME	Q44328 hirudo medi
437	143.5	8.9	458	2	Q61351_MOUSE	Q61351 mus musculu	510	141	8.8	2224	2	Q4SLN7_TETNG	Q4sln7 tetraodon n
438	143.5	8.9	484	2	Q6BE00_XENLA	Q6be00 xenopus lae	511	140.5	8.8	632	2	Q6ZRX5_HUMAN	Q6zrx5 homo sapien
439	143.5	8.9	549	1	PVRL3_MOUSE	Q9j1b9 mus musculu	512	140.5	8.8	810	2	Q9PS96_XENLA	Q9ps96 xenopus lae
440	143.5	8.9	758	2	Q9N2H7_PIG	Q9n2h7 sus scrofa	513	140.5	8.8	946	2	Q07153_TORCA	Q07153 torpedo cal
441	143.5	8.9	998	2	Q495Q3_HUMAN	Q495q3 homo sapien	514	140.5	8.8	1062	2	Q8BKJ3_MOUSE	Q8bkj3 m 15 days e
442	143.5	8.9	1268	2	Q619L9_CAEBR	Q619l9 caenorhabdi	515	140.5	8.8	2170	1	SDK2_HUMAN	Q86ex2 homo sapien
443	143.5	8.9	1386	1	ROB03_HUMAN	Q96ms0 homo sapien	516	140.5	8.8	2623	2	Q6WR10_HUMAN	Q6wr10 mus musculu
444	143.5	8.9	3410	2	Q7TN00_RAT	Q7tn00 rattus norv	517	140.5	8.8	2623	2	Q6WRI0_HUMAN	Q6wri0 homo sapien
445	143	8.9	202	2	Q9NBE1_DROME	Q9nbc1 drosophila	518	140	8.7	340	2	Q61349_MOUSE	Q61349 mus musculu
446	143	8.9	213	2	Q9N167_PAPHA	Q9n167 papio hamad	519	140	8.7	381	2	Q9Y4A4_HUMAN	Q9y4a4 homo sapien
447	143	8.9	231	2	Q9NBB9_DROME	Q9nbb9 drosophila	520	140	8.7	420	2	Q68DM9_HUMAN	Q68dm9 homo sapien
448	143	8.9	413	2	Q6ZNI1_HUMAN	Q6znl1 homo sapien	521	140	8.7	437	2	Q8NF56_HUMAN	Q8nfm6 homo sapien
449	143	8.9	418	2	Q501T5_BRARE	Q501t5 brachydanio	522	140	8.7	591	2	Q8NP04_DROME	Q8np04 drosophila
450	143	8.9	437	2	Q7QG58_ANOGA	Q7qg58 anopheles g	523	140	8.7	977	1	FCRL5_HUMAN	Q96rd9 homo sapien
451	143	8.9	702	1	CEAM5_HUMAN	P06731 homo sapien	524	140	8.7	1261	2	Q4JFL6_RAT	Q4jfl6 rattus norv
452	143	8.9	702	2	Q5G3G0_HUMAN	Q5g3g0 homo sapien	525	140	8.7	1264	2	Q1EBY4_DROME	Q1ebv4 drosophila
453	143	8.9	1114	1	BOC_HUMAN	Q9bvw1 homo sapien	526	140	8.7	1495	2	Q4JFL7_RAT	Q4jfl7 rattus norv
454	143	8.9	1239	2	Q61PF2_CAEBR	Q61pf2 caenorhabdi	527	140	8.7	2016	2	Q8MKM7_DROME	Q8mkm7 drosophila
455	142.5	8.9	226	2	Q4T419_TETNG	Q4t419 tetraodon n	528	140	8.7	2016	2	Q8MKM6_DROME	Q8mkm6 drosophila
456	142.5	8.9	265	1	CEAM7_HUMAN	Q14002 homo sapien	529	140	8.7	2019	2	Q8MKM8_DROME	Q8mkm8 drosophila
457	142.5	8.9	601	2	Q96CJ3_HUMAN	Q96cj3 homo sapien	530	140	8.7	2022	2	Q7KKQ5_DROME	Q7kkq5 drosophila
458	142.5	8.9	824	2	Q4ACB2_BRARE	Q4acb2 brachydanio	531	139.5	8.7	579	2	Q1LZ45_DROME	Q1lza5 drosophila
459	142.5	8.9	1019	2	Q8BJK6_MOUSE	Q8bjk6 m 9 days em	532	139.5	8.7	1150	2	Q2VWPF7_HUMAN	Q2vwp7 homo sapien
460	142.5	8.9	1191	2	Q8EYJ6_MOUSE	Q8eyj6 mus musculu	533	139.5	8.7	1231	2	Q17BD3_AEDAE	Q17bd3 aedes aegyp
461	142.5	8.9	1191	2	Q29VP8_MOUSE	Q29vp8 mus musculu	534	139.5	8.7	1375	2	Q8ML47_DROME	Q8ml47 drosophila
462	142.5	8.9	1256	1	CDON_RAT	Q35158 rattus norv	535	139.5	8.7	1389	2	Q90Z69_BRARE	Q90z69 brachydanio
463	142.5	8.9	1894	1	PTPRD_MOUSE	Q64487 mus musculu	536	139.5	8.7	1419	2	Q98SW3_BRARE	Q98sw3 brachydanio
464	142.5	8.9	1948	1	PTPRS_HUMAN	Q13332 homo sapien	537	139.5	8.7	1526	2	Q9V6D5_DROME	Q9v6d5 drosophila
465	142.5	8.9	3165	2	Q7Q767_ANOGA	Q7q767 anopheles g	538	139.5	8.7	6710	2	Q61SF4_CAEBR	Q61sf4 caenorhabdi
466	142	8.8	291	2	Q28HZ9_XENTR	Q28hz9 xenopus tro	539	139	8.7	324	2	Q7TMH2_MOUSE	Q7tmh2 mus musculu
467	142	8.8	292	2	Q6UY47_HUMAN	Q6uy47 homo sapien	540	139	8.7	332	1	CD22_PANPA	Q9n1e5 pan paniscu
468	142	8.8	335	2	Q5XKA0_XENLA	Q5xka0 xenopus lae	541	139	8.7	332	1	CD22_PANTR	Q9n1e6 pan troglod
469	142	8.8	397	2	Q6XRC3_HUMAN	Q6xrc3 homo sapien	542	139	8.7	336	2	Q80VG4_MOUSE	Q80vg4 mus musculu

543	139	8.7	343	2	Q8R4Y0_MOUSE	Q8r4y0 mus musculus	616	137	8.5	1367	2	Q7PQF4_ANOGA	Q7pqf4 anopheles g
544	139	8.7	399	2	Q8N772_HUMAN	Q8n772 homo sapien	617	137	8.5	1997	2	Q292t1_DROPS	Q292t1 drosophila
545	139	8.7	434	2	Q4RFQ0_TETNG	Q4rfq0 tetraodon n	618	137	8.5	3197	2	Q290B4_DROPS	Q290b4 drosophila
546	139	8.7	477	2	Q5VWES_HUMAN	Q5vwe5 homo sapien	619	136.5	8.5	375	1	Q4S919_TETNG	Q4s919 tetraodon n
547	139	8.7	537	2	Q5VTD4_HUMAN	Q5vtd4 homo sapien	620	136.5	8.5	394	1	IGS4B_XENLA	Q7xx1 xenopus lae
548	139	8.7	553	2	Q8WXJ5_HUMAN	Q8wxj5 homo sapien	621	136.5	8.5	459	2	Q4RS41_TETNG	Q4rs41 tetraodon n
549	139	8.7	602	2	Q86XJ9_HUMAN	Q86xj9 homo sapien	622	136.5	8.5	476	2	Q3UHE3_MOUSE	Q3uhe3 mus musculus
550	139	8.7	650	2	Q8NA84_HUMAN	Q8na84 homo sapien	623	136.5	8.5	814	2	Q28J96_XENTR	Q28j96 xenopus tro
551	139	8.7	781	1	Q59GJ1_HUMAN	Q59gj1 homo sapien	624	136.5	8.5	821	1	NTRK2_MOUSE	P15209 mus musculus
552	139	8.7	822	1	NTRK2_HUMAN	Q16620 homo sapien	625	136.5	8.5	1086	2	Q172F7_AEDAE	Q172f7 aedes aegyp
553	139	8.7	822	2	Q5VVP4_HUMAN	Q5vvp4 homo sapien	626	136.5	8.5	1328	2	Q4RKW3_TETNG	Q4rkW3 tetraodon n
554	139	8.7	828	2	Q8WXJ7_HUMAN	Q8wxj7 homo sapien	627	136	8.5	361	2	Q1LUH5_BRARE	Q1luh5 brachydanio
555	139	8.7	1225	2	Q6GP61_XENLA	Q6gp61 xenopus lae	628	136	8.5	416	2	Q67IP8_HUMAN	Q67ip8 homo sapien
556	139	8.7	1348	2	Q677M1_CHICK	Q677m1 gallus gall	629	136	8.5	500	1	BTNL8_HUMAN	Q6ux41 homo sapien
557	139	8.7	1759	2	Q7PPH8_ANOGA	Q7pph8 anopheles g	630	136	8.5	941	2	Q4SMD8_TETNG	Q4smd8 tetraodon n
558	138.5	8.6	278	2	Q9OYL3_MOUSE	Q9oYl3 mus musculus	631	136	8.5	945	2	Q29HP2_DROPS	Q29hp2 drosophila
559	138.5	8.6	330	2	Q90242_CHICK	Q90242 gallus gall	632	136	8.5	1270	2	Q9U3P2_CAEL	Q9u3p2 caenorhabdi
560	138.5	8.6	344	1	NTRL_MOUSE	Q99fp10 mus musculus	633	136	8.5	1478	2	Q59H90_HUMAN	Q59h90 homo sapien
561	138.5	8.6	344	2	Q8BG33_MOUSE	Q8bg33 m adult mal	634	136	8.5	1906	1	MYLK_CHICK	Q91799 gallus gall
562	138.5	8.6	344	2	Q3TYC2_MOUSE	Q3tyc2 mus musculus	635	135.5	8.4	326	2	Q9N166_PAPHA	Q9n166 papio hamad
563	138.5	8.6	508	2	Q8CED8_MOUSE	Q8ced8 mus musculus	636	135.5	8.4	484	2	Q5QSL1_XENTR	Q5qsl1 xenopus tro
564	138.5	8.6	1375	2	Q94537_DROME	Q94537 drosophila	637	135.5	8.4	563	2	Q5FWR8_XENTR	Q5fwr8 xenopus tro
565	138.5	8.6	1526	2	Q94538_DROME	Q94538 drosophila	638	135.5	8.4	587	2	Q1W3D1_PIG	Q1w3d1 sus scrofa
566	138	8.6	283	2	Q7PCU3_ANOGA	Q7pcu3 anopheles g	639	135.5	8.4	881	2	Q60UL6_CAEBR	Q60ul6 caenorhabdi
567	138	8.6	283	2	Q5TNQ2_ANOGA	Q5tnq2 anopheles g	640	135.5	8.4	1010	1	CNTN1_CHICK	P14781 gallus gall
568	138	8.6	379	1	JAML1_MOUSE	Q80u19 mus musculus	641	135.5	8.4	1030	2	Q8NFA8_HUMAN	Q8nfa8 homo sapien
569	138	8.6	389	2	Q2VPF6_XENLA	Q2vpf6 xenopus lae	642	135.5	8.4	1227	2	Q21038_CAEL	Q21038 caenorhabdi
570	138	8.6	393	2	Q16Q42_AEDAE	Q16q42 aedes aegyp	643	135.5	8.4	1843	2	Q4SPF7_TETNG	Q4spf7 tetraodon n
571	138	8.6	393	2	Q5E9Z9_BOVIN	Q5e9z9 bos taurus	644	135.5	8.4	2233	2	Q4T1M4_TETNG	Q4t1m4 tetraodon n
572	138	8.6	796	2	Q91287_PLEWA	Q91287 pleurodeles	645	135	8.4	238	2	Q5YJ11_SHEEP	Q5yji1 oviv aries
573	138	8.6	804	2	Q800Z1_BRARE	Q800z1 brachydanio	646	135	8.4	281	1	NPTN_MOUSE	P97300 mus musculus
574	138	8.6	804	2	Q90200_BRARE	Q90200 brachydanio	647	135	8.4	281	1	NPTN_MOUSE	P97300 mus musculus
575	138	8.6	1919	2	Q1T6Y3_APIME	Q1t6y3 apis mellif	648	135	8.4	302	2	O5YJ10_SHEEP	O5yji0 ovis aries
576	138	8.6	2772	2	Q9VAV4_DROME	Q9vav4 drosophila	649	135	8.4	337	1	OBCAM_CHICK	Q38892 gallus gall
577	138	8.6	2894	2	Q7KRX2_DROSOPHILA	Q7kx2 drosophila	650	135	8.4	338	1	LSAMP_HUMAN	Q33449 homo sapien
578	137.5	8.6	279	2	Q2XQV0_MOUSE	Q2xqv0 mus musculus	651	135	8.4	344	2	Q9DF61_CHICK	Q9df61 gallus gall
579	137.5	8.6	282	1	NPTN_HUMAN	Q9y639 homo sapien	652	135	8.4	367	2	Q6ZWL4_HUMAN	Q6zwl4 homo sapien
580	137.5	8.6	282	2	Q17R52_HUMAN	Q17r52 homo sapien	653	135	8.4	461	2	Q13854_HUMAN	Q13854 homo sapien
581	137.5	8.6	396	2	Q17QV6_BOVIN	Q17qv6 bos taurus	654	135	8.4	461	2	Q4SMF3_TETNG	Q4smf3 tetraodon n
582	137.5	8.6	416	2	Q8N713_HUMAN	Q8n713 homo sapien	655	135	8.4	2776	2	Q869A0_DROME	Q869a0 drosophila
583	137.5	8.6	509	2	Q91YK7_MOUSE	Q91yk7 mus musculus	656	135	8.4	2898	2	Q868Z9_DROME	Q868z9 drosophila
584	137.5	8.6	528	2	P91670_DROME	P91670 drosophila	657	134.5	8.4	214	2	Q4SX01_TETNG	Q4sx01 tetraodon n
585	137.5	8.6	536	2	Q4V5E0_DROME	Q4v5e0 drosophila	658	134.5	8.4	290	1	PDL1_HUMAN	Q9nzb7 homo sapien
586	137.5	8.6	545	2	Q9VCT4_DROME	Q9vct4 drosophila	659	134.5	8.4	316	1	CD276_RAT	Q7tpb4 rattus norv
587	137.5	8.6	549	1	PVRL3_HUMAN	Q9nq3 homo sapien	660	134.5	8.4	322	1	ICOSL_MOUSE	Q9jhj8 mus musculus
588	137.5	8.6	551	2	Q8MEN7_DROME	Q8men7 drosophila	661	134.5	8.4	322	2	Q544C7_MOUSE	Q544c7 mus musculus
589	137.5	8.6	606	2	Q9VMN6_DROME	Q9vmn6 drosophila	662	134.5	8.4	368	2	Q5ZJK6_CHICK	Q5zjk6 gallus gall
590	137.5	8.6	709	2	Q81XC7_HUMAN	Q81xc7 homo sapien	663	134.5	8.4	620	2	Q17F26_AEDAE	Q17f26 aedes aegyp
591	137.5	8.6	800	2	Q86LF9_DROVI	Q86lf9 drosophila	664	134.5	8.4	676	2	Q4SIF9_TETNG	Q4sif9 tetraodon n
592	137.5	8.6	800	2	Q9JHX9_RAT	Q9jhx9 rattus norv	665	134.5	8.4	677	2	Q16G95_AEDAE	Q16g95 aedes aegyp
593	137.5	8.6	801	2	Q86LF8_DROVI	Q86lf8 drosophila	666	134.5	8.4	682	2	Q16G95_AEDAE	Q16g95 aedes aegyp
594	137.5	8.6	956	2	Q9W4T9_DROME	Q9w4t9 drosophila	667	134.5	8.4	761	2	Q95LQ2_WACFA	Q95lq2 macaca fasc
595	137.5	8.6	959	2	Q9N9Y9_DROME	Q9n9y9 drosophila	668	134.5	8.4	814	2	Q91897_XENLA	Q91897 xenopus lae
596	137.5	8.6	975	2	Q97174_DROME	Q97174 drosophila	669	134.5	8.4	821	1	NTRK2_RAT	Q63604 rattus norv
597	137.5	8.6	1000	2	Q4TBR4_TETNG	Q4tbr4 tetraodon n	670	134.5	8.4	1028	1	CNTN3_MOUSE	Q7409 mus musculus
598	137.5	8.6	1249	2	Q7FMZ9_RAT	Q7fmz9 rattus norv	671	134.5	8.4	1336	1	VGFR1_MOUSE	P53767 rattus norv
599	137.5	8.6	1280	2	Q90933_CHICK	Q90933 gallus gall	672	134	8.3	343	2	Q8BYS4_MOUSE	Q8bys4 mus musculus
600	137.5	8.6	1946	2	Q6BU72_APIME	Q6bu72 apis mellif	673	134	8.3	698	2	Q5TN75_ANOGA	Q5tn75 anopheles g
601	137.5	8.6	6225	2	Q7PUW6_ANOGA	Q7puw6 anopheles g	674	134	8.3	747	2	Q5DTZ4_MOUSE	Q5dtz4 mus musculus
602	137	8.5	267	2	Q8NC05_HUMAN	Q8nc05 homo sapien	675	134	8.3	778	1	KIRK3_MOUSE	Q8br86 mus musculus
603	137	8.5	391	2	Q4S871_TETNG	Q4s871 tetraodon n	676	134	8.3	868	1	MUSK_RAT	Q62838 rattus norv
604	137	8.5	474	2	Q5FV48_FUGRU	Q5fv48 fugu rubrip	677	134	8.3	954	2	Q7PV74_ANOGA	Q7pv74 anopheles g
605	137	8.5	526	1	BTAL_BOVIN	P18892 bos taurus	678	134	8.3	1023	2	Q9ULI7_HUMAN	Q9uli7 homo sapien
606	137	8.5	570	2	Q8NCE6_HUMAN	Q8nce6 homo sapien	679	134	8.3	1285	2	Q17DL2_AEDAE	Q17dl2 aedes aegyp
607	137	8.5	613	2	Q7PX10_ANOGA	Q7px10 anopheles g	680	134	8.3	1460	2	Q17DP1_AEDAE	Q17dp1 aedes aegyp
608	137	8.5	784	2	Q81063_DROVI	Q81063 drosophila	681	134	8.3	5505	2	Q4RU89_TETNG	Q4ru89 tetraodon n
609	137	8.5	910	2	Q179P1_AEDAE	Q179p1 aedes aegyp	682	133.5	8.3	265	2	Q81PQ9_DROME	Q81pq9 drosophila
610	137	8.5	913	2	Q813E5_CAEL	Q8t3e5 caenorhabdi	683	133.5	8.3	298	2	Q96114_HUMAN	Q96114 drosophila
611	137	8.5	928	2	Q19128_CAEL	Q19128 caenorhabdi	684	133.5	8.3	348	2	Q00557_HUMAN	O00557 homo sapien
612	137	8.5	1164	2	Q66MN5_DROVI	Q66mn5 drosophila	685	133.5	8.3	812	1	FGFR1_XENLA	P22182 xenopus lae
613	137	8.5	1249	1	CDON_XENLA	Q90z04 xenopus lae	686	133.5	8.3	816	2	Q8NFA5_HUMAN	Q8nfa5 homo sapien
614	137	8.5	1272	2	Q5GIT3_BRARE	Q5git3 brachydanio	687	133.5	8.3	948	2	Q9VME2_DROME	Q9vme2 drosophila
615	137	8.5	1566	1	ROBO3_MOUSE	Q92214 mus musculus	688	133.5	8.3	1070	2	Q6IQ54_HUMAN	Q6iq54 homo sapien

689	133.5	8.3	1070	2	Q5T650_HUMAN	Q5T650 homo sapien	762	131.5	8.2	778	1	KIRR3_HUMAN	O8izu9 homo sapien
690	133.5	8.3	1427	2	Q91562_XENLA	Q91562 xenopus lae	763	131.5	8.2	778	2	Q3MLJ7_HUMAN	Q3mlj7 homo sapien
691	133.5	8.3	4071	2	Q7PH68_ANOGA	Q7PH68 anopheles g	764	131.5	8.2	786	2	Q4SR20_TETNG	Q4sr20 tetraodon n
692	133.5	8.3	4098	2	Q7POG9_ANOGA	Q7POG9 anopheles g	765	131.5	8.2	900	2	Q4SR23_TETNG	Q4sr23 tetraodon n
693	133	8.3	289	2	Q9GYL5_MOUSE	Q9GYL5 mus musculus	766	131.5	8.2	1006	2	Q6IDE9_DROME	Q6ide9 drosophila
694	133	8.3	305	2	Q6P3A4_MOUSE	Q6P3A4 mus musculus	767	131.5	8.2	1140	2	Q4RRD1_TETNG	Q4rrd1 tetraodon n
695	133	8.3	311	2	Q6DN73_HUMAN	Q6dn73 homo sapien	768	131.5	8.2	1387	2	Q4SQO2_TETNG	Q4sq3 tetraodon n
696	133	8.3	334	2	Q02870_CHICK	Q02870 gallus gall	769	131	8.2	197	2	Q2VA88_DROME	Q2va88 drosophila
697	133	8.3	338	1	LSAMP_CHICK	Q98919 gallus gall	770	131	8.2	197	2	Q2VA98_DROME	Q2va98 drosophila
698	133	8.3	338	1	LSAMP_RAT	Q62813 rattus norv	771	131	8.2	197	2	Q2VAC5_DROME	Q2vac5 drosophila
699	133	8.3	377	2	Q4RZV7_TETNG	Q4rzv7 tetraodon n	772	131	8.2	295	2	Q9QYL6_MOUSE	Q9qyl6 mus musculus
700	133	8.3	459	2	Q9JHL6_RAT	Q9jhl6 rattus norv	773	131	8.2	366	2	Q8N759_HUMAN	Q8n759 homo sapien
701	133	8.3	639	2	Q96P30_HUMAN	Q96p30 homo sapien	774	131	8.2	463	2	Q640R3_MOUSE	Q640r3 mus musculus
702	133	8.3	683	2	Q173C9_AEDAE	Q173c9 aedes aegyp	775	131	8.2	554	2	Q9W4R3_DROME	Q9w4r3 drosophila
703	133	8.3	707	2	Q5VXZ8_HUMAN	Q5vxz8 homo sapien	776	131	8.2	771	1	PICR_MOUSE	Q70570 mus musculus
704	133	8.3	734	2	Q96P31_HUMAN	Q96p31 homo sapien	777	131	8.2	817	2	Q4H2M8_CIOIN	Q4h2m8 ciona intes
705	133	8.3	734	2	Q961A4_HUMAN	Q961a4 homo sapien	778	131	8.2	870	2	Q7PVG1_ANOGA	Q7pvg1 anopheles g
706	133	8.3	742	2	Q8N6S2_HUMAN	Q8n6s2 homo sapien	779	131	8.2	1036	1	CNTN2_CHICK	P28885 gallus gall
707	133	8.3	919	1	UNC5_CABEL	Q26261 caenorhabdi	780	131	8.2	1043	2	Q6PA07_XENLA	Q6pa07 xenopus lae
708	133	8.3	955	1	MDGAI_HUMAN	Q8nfp4 homo sapien	781	131	8.2	1252	2	Q9JLI1_MOUSE	Q9jli1 mus musculus
709	133	8.3	1065	1	LRIG2_HUMAN	Q94898 homo sapien	782	131	8.2	1428	2	Q8AY67_BRARE	Q8ay67 brachydanio
710	133	8.3	1125	2	Q1LYF7_BRARE	Q1lyf7 brachydanio	783	131	8.2	1896	2	Q9IAJ1_XENLA	Q9iaj1 xenopus lae
711	133	8.3	1177	2	Q6QGB1_XENLA	Q6qgb1 xenopus lae	784	130.5	8.1	91	2	Q91667_XENLA	Q91667 xenopus lae
712	133	8.3	1990	2	Q16SD7_AEDAE	Q16sd7 aedes aegyp	785	130.5	8.1	208	2	Q80WN3_MOUSE	Q80wn3 mus musculus
713	133	8.3	2213	1	SDK1_HUMAN	Q175n4 homo sapien	786	130.5	8.1	262	1	TMIGD_HUMAN	Q6uxz6 xenopus lae
714	132.5	8.3	309	2	Q91YV7_MOUSE	Q91yv7 mus musculus	787	130.5	8.1	292	2	Q5HZR6_XENLA	Q5hzz6 mus musculus
715	132.5	8.3	312	2	Q4SNG2_TETNG	Q4sng2 tetraodon n	788	130.5	8.1	300	2	Q68SP0_MOUSE	Q68sp0 mus musculus
716	132.5	8.3	337	2	Q6GLZ7_XENLA	Q6glz7 xenopus lae	789	130.5	8.1	316	2	Q5F3J1_CHICK	Q5f3j1 gallus gall
717	132.5	8.3	389	2	Q3TQJ7_MOUSE	Q3tqj1 m adult mal	790	130.5	8.1	349	2	Q7QJG1_ANOGA	Q7qjg1 anopheles g
718	132.5	8.3	416	2	Q7QJL7_RAT	Q7qjz7 anopheles g	791	130.5	8.1	368	2	Q2ABP7_EPTBU	Q2abp7 eptaretus
719	132.5	8.3	448	2	Q9JHL7_RAT	Q9jhl7 rattus norv	792	130.5	8.1	429	2	Q9GPF6_HUMAN	Q9gpf6 homo sapien
720	132.5	8.3	762	2	Q3TQL1_MOUSE	Q3tql1 mus musculus	793	130.5	8.1	429	2	Q961A6_HUMAN	Q961a6 homo sapien
721	132.5	8.3	800	2	Q7FSI8_MOUSE	Q7fsi8 mus musculus	794	130.5	8.1	442	2	Q8C306_MOUSE	Q8c306 mus musculus
722	132.5	8.3	800	2	Q9S052_MOUSE	Q9s052 mus musculus	795	130.5	8.1	484	2	Q26475_SCHAM	Q26475 schistocerc
723	132.5	8.3	801	1	FGR3_MOUSE	Q61851 mus musculus	796	130.5	8.1	487	1	FGR1_CHICK	Q7t2h2 gallus gall
724	132.5	8.3	801	2	Q3UPEI_MOUSE	Q3upe1 mus musculus	797	130.5	8.1	492	2	Q9ET54_MOUSE	Q9et54 mus musculus
725	132.5	8.3	814	1	PUNC_HUMAN	Q81vul homo sapien	798	130.5	8.1	538	2	Q29123_PIG	Q29123 sus scrofa
726	132.5	8.3	920	2	Q4RSG7_TETNG	Q4rsq7 tetraodon n	799	130.5	8.1	807	2	Q6NY23_BRARE	Q6ny23 brachydanio
727	132.5	8.3	949	2	Q4SL83_TETNG	Q4sl83 tetraodon n	800	130.5	8.1	853	2	Q6DPX7_MOUSE	Q6dpf7 mus musculus
728	132.5	8.3	1099	1	CNTN5_RAT	Q95527 rattus norv	801	130.5	8.1	940	2	Q8NFA7_HUMAN	Q8nfa7 homo sapien
729	132.5	8.3	1133	2	Q4T6R9_TETNG	Q4t6r9 tetraodon n	802	130.5	8.1	1015	2	Q4SNF9_TETNG	Q4snf9 tetraodon n
730	132.5	8.3	1209	2	Q4SF88_TETNG	Q4sf88 tetraodon n	803	130.5	8.1	1027	2	Q9VFU7_DROME	Q9vfu7 drosophila
731	132.5	8.3	1304	2	Q9VBE5_DROME	Q9vbe5 drosophila	804	130.5	8.1	1081	2	Q69ZT7_MOUSE	Q69zt7 mus musculus
732	132.5	8.3	1356	1	VGRF2_HUMAN	P35968 homo sapien	805	130.5	8.1	1098	1	CNTN5_MOUSE	P68500 mus musculus
733	132.5	8.3	1451	2	Q59EB0_HUMAN	O59eb0 homo sapien	806	130.5	8.1	1192	2	Q610E4_CABER	Q610e4 caenorhabdi
734	132	8.2	334	2	Q17G58_AEDAE	Q17g58 aedes aegyp	807	130.5	8.1	1379	2	Q28YX8_DROPS	Q28yx8 drosophila
735	132	8.2	338	2	Q3TYE5_MOUSE	Q3tye5 mus musculus	808	130.5	8.1	2174	2	Q9GQR0_DROME	Q9gqr0 drosophila
736	132	8.2	510	2	Q6EH12_RAT	Q6eh12 rattus norv	809	130.5	8.1	2177	1	SDK2_CHICK	Q8av37 gallus gall
737	132	8.2	597	2	Q1LXV7_BRARE	Q1lxv7 brachydanio	810	130	8.1	263	2	Q3V2W2_MOUSE	Q3v2w2 mus musculus
738	132	8.2	1070	1	PTK7_HUMAN	Q13308 homo sapien	811	130	8.1	303	2	Q7ZXR4_XENLA	Q7zxr4 xenopus lae
739	132	8.2	1262	2	Q17EB4_AEDAE	Q17eb4 aedes aegyp	812	130	8.1	320	2	Q4V8Z8_XENLA	Q4v8z8 xenopus lae
740	132	8.2	1272	2	Q4JDD5_BRARE	Q4jdd5 brachydanio	813	130	8.1	321	2	Q32NA7_XENLA	Q32na7 xenopus lae
741	132	8.2	1333	1	VGFR1_MOUSE	P35969 mus musculus	814	130	8.1	341	1	Q6INF0_XENLA	Q6inf0 xenopus lae
742	132	8.2	1348	1	VGFR2_COTUA	P52583 coturnix co	815	130	8.1	343	2	Q17DU8_AEDAE	Q17du8 aedes aegyp
743	132	8.2	1363	1	VGFR3_RAT	Q91121 rattus norv	816	130	8.1	458	2	Q7PW77_ANOGA	Q7pw77 anopheles g
744	132	8.2	1870	2	Q16J84_AEDAE	Q16j84 aedes aegyp	817	130	8.1	618	2	Q16ZD1_AEDAE	Q16zd1 aedes aegyp
745	132	8.2	1841	1	MYLK_MOUSE	Q6pdn3 mus musculus	818	130	8.1	783	2	Q32MJ9_HUMAN	Q32mj9 homo sapien
746	132	8.2	2024	2	Q53CM6_BRARE	Q53cm6 brachydanio	819	130	8.1	802	2	Q95M13_BOVIN	Q95m13 bos taurus
747	132	8.2	2222	2	Q4RY92_TETNG	Q4ry92 tetraodon n	820	130	8.1	885	2	Q8HYV1_PIG	Q8hyv1 sus scrofa
748	132	8.2	4736	2	Q7YT99_MYTGA	Q7yt99 mytilus gal	821	130	8.1	886	2	Q8HYV2_PIG	Q8hyv2 sus scrofa
749	131.5	8.2	175	2	Q4TYG2_TETNG	Q4tyg2 tetraodon n	822	130	8.1	912	2	Q4S2G4_TETNG	Q4s2g4 tetraodon n
750	131.5	8.2	293	2	Q3JUE8_MOUSE	Q3jue8 mus musculus	823	130	8.1	1198	2	Q7QD44_ANOGA	Q7qdd4 anopheles g
751	131.5	8.2	306	2	Q9R1Z9_MOUSE	Q9riz9 mus musculus	824	130	8.1	1345	1	NTRI_BOVIN	Q9n168 papio hamad
752	131.5	8.2	309	1	CD86_MOUSE	P42082 mus musculus	825	129.5	8.1	292	2	Q9N168_PAPHA	Q9ndas bos taurus
753	131.5	8.2	309	2	Q54Q29_MOUSE	Q54q29 mus musculus	826	129.5	8.1	345	1	Q17QT6_BOVIN	Q17qt6 bos taurus
754	131.5	8.2	314	2	Q61238_MOUSE	Q61238 mus musculus	827	129.5	8.1	345	2	Q5W960_RAT	Q5w960 rattus norv
755	131.5	8.2	344	1	NTRI_HUMAN	Q9p121 homo sapien	828	129.5	8.1	361	2	Q5RJW1_MOUSE	Q5rjw1 mus musculus
756	131.5	8.2	344	2	Q5R554_PONPY	Q5r554 pongo pygma	829	129.5	8.1	661	1	PUNC_MOUSE	Q8bq3 mus musculus
757	131.5	8.2	356	2	Q64381_MOUSE	Q64381 mus musculus	830	129.5	8.1	813	1	Q1JUB6_DUGUA	Q1jub6 dugesia jap
758	131.5	8.2	358	2	Q16W85_AEDAE	Q16w85 aedes aegyp	831	129.5	8.1	843	2	Q58EP4_BRARE	Q58ep4 brachydanio
759	131.5	8.2	538	2	Q28939_PIG	Q28939 sus scrofa	832	129.5	8.1	1095	2	Q58EP4_BRARE	Q58ep4 brachydanio
760	131.5	8.2	648	1	MUC18_RAT	Q9epf2 rattus norv	833	129.5	8.1	1117	1	LRIG3_MOUSE	Q6p166 mus musculus
761	131.5	8.2	747	2	Q4H3K6_CIOIN	Q4h3k6 ciona intes	834	129.5	8.1	2127	2	Q29A88_DROPS	Q29a88 drosophila

835	129	8.0	276	2	Q6P0R7_BRARE	Q6P0r7 brachydanio	908	128	8.0	1363	2	Q5SU94_MOUSE	Q5su94 mus musculus
836	129	8.0	295	2	Q9Z2H8_MOUSE	Q9z2h8 mus musculus	909	128	8.0	1409	2	Q8J127_BRARE	Q8j127 brachydanio
837	129	8.0	308	2	Q5O3N7_BRARE	Q5o3n7 brachydanio	910	128	8.0	1409	2	Q8O1M2_BRARE	Q8o1m2 brachydanio
838	129	8.0	338	2	Q6DH44_BRARE	Q6dh44 brachydanio	911	128	8.0	2095	2	Q4S8U5_TETNG	Q4s8u5 tetraodon n
839	129	8.0	343	2	Q4SDU6_TETNG	Q4sdu6 tetraodon n	912	128	8.0	4648	2	Q4T3W5_TETNG	Q4t3w5 tetraodon n
840	129	8.0	350	2	O02869_CHICK	O02869 gallus gall	913	127.5	7.9	249	2	Q58DG9_BOVIN	Q58dg9 bos taurus
841	129	8.0	448	2	O81GAS_DROME	O81gas drosophila	914	127.5	7.9	316	1	CD276_MOUSE	Q8ve98 mus musculus
842	129	8.0	537	2	Q70EY8_ANOGA	Q70ey8 anopheles g	915	127.5	7.9	622	2	Q3TAG1_MOUSE	Q3tag1 mus musculus
843	129	8.0	577	2	Q80Y42_MOUSE	Q80y42 mus musculus	916	127.5	7.9	905	2	Q4RLG1_TETNG	Q4rlg1 tetraodon n
844	129	8.0	650	2	Q9GKR2_BOVIN	Q9gkr2 bos taurus	917	127.5	7.9	947	1	MUSK_CHICK	Q8axy6 gallus gall
845	129	8.0	685	2	Q2TAE7_XENLA	Q2tae7 xenopus lae	918	127.5	7.9	1149	2	Q2EV14_BRARE	Q2ev14 brachydanio
846	129	8.0	700	1	K1RR2_MOUSE	Q7tsu7 mus musculus	919	127.5	7.9	1232	2	Q90284_CARAU	Q90284 carassius a
847	129	8.0	723	2	Q5HZF8_XENLA	Q5hzf8 xenopus lae	920	127.5	7.9	1238	2	Q58QC3_XENLA	Q58qc3 xenopus lae
848	129	8.0	727	2	Q5W5X8_XENLA	Q5w5x8 xenopus lae	921	127.5	7.9	1845	2	Q5MYA0_HUMAN	Q5mya0 homo sapien
849	129	8.0	769	1	PIGR_RAT	P15083 rattus norv	922	127.5	7.9	1914	2	Q5MY99_HUMAN	Q5my99 homo sapien
850	129	8.0	782	2	Q4SI43_TETNG	Q4si43 tetraodon n	923	127.5	7.9	1914	2	Q7Z4J0_HUMAN	Q7z4j0 homo sapien
851	129	8.0	867	2	Q5VZM7_HUMAN	Q5vzm7 homo sapien	924	127.5	7.9	2169	1	SDK1_CHICK	Q8av58 gallus gall
852	129	8.0	875	2	Q5VZW8_HUMAN	Q5vzw8 homo sapien	925	127	7.9	204	2	Q7PJY5_ANOGA	Q7pjy5 anopheles g
853	129	8.0	957	2	Q5TF58_HUMAN	Q5tf58 homo sapien	926	127	7.9	349	1	LACH_SCHAM	Q26474 schistocerc
854	129	8.0	1027	1	CNTN6_RAT	Q90w79 gallus gall	927	127	7.9	504	1	FGRL1_HUMAN	Q8n441 homo sapien
855	129	8.0	1028	1	O5RM6_MOUSE	P97528 rattus norv	928	127	7.9	577	2	Q9D221_MOUSE	Q9d221 m adult mal
856	129	8.0	1100	2	Q9QSQ9_MOUSE	Q9rk8 mus musculus	929	127	7.9	782	2	Q61563_MOUSE	Q61563 mus musculus
857	129	8.0	1252	2	Q9QSQ9_MOUSE	Q9eq9 mus musculus	930	127	7.9	1012	2	Q4SW91_TETNG	Q4sw91 tetraodon n
858	129	8.0	1253	2	Q9BQS8_MOUSE	Q9eqs8 mus musculus	931	127	7.9	1753	2	Q2M0G8_DROPS	Q2m0g8 drosophila
859	129	8.0	1269	2	Q6U715_BRARE	Q6u715 brachydanio	932	127	7.9	3262	1	SPEG_MOUSE	Q62407 mus musculus
860	129	8.0	1311	2	Q9V1K8_DROME	Q9v1k8 drosophila	933	127	7.9	4604	2	Q17AF2_AEDAE	Q17af2 aedes aegyp
861	129	8.0	1527	2	O9VZ24_DROME	Q9vz24 drosophila	934	126.5	7.9	231	2	Q8WYV6_HUMAN	Q8wyv6 homo sapien
862	129	8.0	1535	2	Q23991_DROME	Q23991 drosophila	935	126.5	7.9	269	2	Q16E78_AEDAE	Q16e78 aedes aegyp
863	129	8.0	6048	2	Q7JN85_CABEL	Q7jnh5 caenorhabdi	936	126.5	7.9	306	1	CD80_MOUSE	Q00609 mus musculus
864	129	8.0	6101	2	Q7PXW9_ANOGA	Q7pxw9 anopheles g	937	126.5	7.9	306	2	Q549R2_MOUSE	Q549r2 mus musculus
865	129	8.0	6839	2	Q23550_CABEL	Q23550 caenorhabdi	938	126.5	7.9	333	2	Q2EGT7_BRARE	Q2egt7 brachydanio
866	129	8.0	7158	2	Q23551_CABEL	Q23551 caenorhabdi	939	126.5	7.9	333	1	CEPU1_CHICK	Q90773 gallus gall
867	129	8.0	17352	2	Q95YM2_PROCL	Q95ym2 procambarus	940	126.5	7.9	410	2	Q3TOK2_MOUSE	Q3tok2 mus musculus
868	128.5	8.0	272	2	Q8RLN5_MOUSE	Q8rln5 mus musculus	941	126.5	7.9	419	1	PSG4_HUMAN	Q00688 homo sapien
869	128.5	8.0	274	2	Q4W5Q0_HUMAN	Q4w5q0 homo sapien	942	126.5	7.9	419	1	PSG7_HUMAN	Q13046 homo sapien
870	128.5	8.0	294	2	Q8GWE8_HUMAN	Q8gwe8 homo sapien	943	126.5	7.9	419	2	Q96QL5_HUMAN	Q96ql5 homo sapien
871	128.5	8.0	309	2	Q3T9F8_MOUSE	Q3t9f8 mus musculus	944	126.5	7.9	419	2	Q6P520_HUMAN	Q6p520 homo sapien
872	128.5	8.0	325	2	Q5O1V7_BRARE	Q5o1v7 brachydanio	945	126.5	7.9	450	2	Q9VR25_DROME	Q9vr25 drosophila
873	128.5	8.0	360	2	Q8MRE6_DROME	Q8mre6 drosophila	946	126.5	7.9	1026	1	CNTM4_MOUSE	Q69z26 mus musculus
874	128.5	8.0	409	2	Q3V5D4_XENLA	Q3v5d4 xenopus lae	947	126.5	7.9	1083	2	Q76698_CABEL	Q76698 caenorhabdi
875	128.5	8.0	480	2	Q9PSC9_9PIPI	Q9psc9 xenopus. fi	948	126.5	7.9	1447	1	DCC_HUMAN	P43146 homo sapien
876	128.5	8.0	510	2	Q7L3E0_HUMAN	Q7l3e0 homo sapien	949	126.5	7.9	1515	2	Q4SHH6_TETNG	Q4shh6 tetraodon n
877	128.5	8.0	719	2	Q9U4G1_DROME	Q9u4g1 drosophila	950	126.5	7.9	2095	2	Q4RYE5_TETNG	Q4rye5 tetraodon n
878	128.5	8.0	757	1	PIGR_BOVIN	P81265 bos taurus	951	126	7.9	190	2	Q4SA11_TETNG	Q4sa11 tetraodon n
879	128.5	8.0	764	2	Q5RA58_PONPY	Q5ra58 pongo pygma	952	126	7.9	261	1	TMIGD_MOUSE	Q9d718 mus musculus
880	128.5	8.0	764	2	Q5RDC2_PONPY	Q5rdc2 pongo pygma	953	126	7.9	465	2	Q59E14_DROME	Q59e14 drosophila
881	128.5	8.0	772	2	Q9Y2J6_HUMAN	Q9y2j6 homo sapien	954	126	7.9	600	2	Q1LUP9_BRARE	Q1lup9 brachydanio
882	128.5	8.0	793	2	Q4RFN0_TETNG	Q4rfn0 tetraodon n	955	126	7.9	878	2	Q497X0_MOUSE	Q497x0 mus musculus
883	128.5	8.0	814	2	Q6GNP8_XENLA	Q6gnp8 xenopus lae	956	126	7.9	878	2	Q32SD3_MOUSE	Q32sd3 mus musculus
884	128.5	8.0	893	2	Q3UQU8_MOUSE	Q3uq8 mus musculus	957	126	7.9	881	2	Q4RQ3_TETNG	Q4rq3 tetraodon n
885	128.5	8.0	893	2	Q3TRES_MOUSE	Q3tres mus musculus	958	126	7.9	893	2	Q32SD4_MOUSE	Q32sd4 mus musculus
886	128.5	8.0	937	2	Q5WN68_CABER	Q5wn68 caenorhabdi	959	126	7.9	1019	2	Q16XM4_AEDAE	Q16xm4 aedes aegyp
887	128.5	8.0	1056	1	CNTN5_BRARE	Q7zw34 brachydanio	960	126	7.9	1028	1	CNTNG_HUMAN	Q9u52 homo sapien
888	128.5	8.0	1098	2	Q4RR11_TETNG	Q4rrt1 tetraodon n	961	126	7.9	1028	1	CNTNG_MOUSE	Q9jmb8 mus musculus
889	128.5	8.0	1106	2	Q8WX93_HUMAN	Q8wx93 homo sapien	962	126	7.9	1028	2	Q2KHM2_HUMAN	Q2khm2 homo sapien
890	128.5	8.0	1182	2	Q16Z16_AEDAE	Q16z16 aedes aegyp	963	126	7.9	1028	2	Q5RGD4_PONPY	Q5rgd4 pongo pygma
891	128.5	8.0	1914	1	MYLK_HUMAN	Q15746 homo sapien	964	126	7.9	1338	1	VGFR1_HUMAN	P17948 homo sapien
892	128.5	8.0	2224	1	SDK_DROME	Q97394 drosophila	965	126	7.9	1338	2	Q5TAR1_ANOGA	Q5tar1 homo sapien
893	128.5	8.0	2752	2	Q7QKD0_ANOGA	Q7qkd0 anopheles g	966	126	7.9	1400	2	Q7PF94_HUMAN	Q7pf94 anopheles g
894	128.5	8.0	4447	2	Q8MXD8_CABEL	Q8mxd8 caenorhabdi	967	125.5	7.8	276	2	Q16ML7_AEDAE	Q16ml7 aedes aegyp
895	128	8.0	298	2	Q17BD7_AEDAE	Q17bd7 aedes aegyp	968	125.5	7.8	282	2	Q7Z7D3_HUMAN	Q7z7d3 homo sapien
896	128	8.0	403	2	Q6NZV3_BRARE	Q6nzv3 brachydanio	969	125.5	7.8	285	2	Q5T2L0_HUMAN	Q5t2l0 homo sapien
897	128	8.0	411	2	Q7QGM5_ANOGA	Q7qgm5 anopheles g	970	125.5	7.8	288	2	Q16ML6_AEDAE	Q16ml6 aedes aegyp
898	128	8.0	450	2	Q3LFS5_MOUSE	Q3lfs5 mus musculus	971	125.5	7.8	299	2	Q7QMP9_ANOGA	Q7qmp9 anopheles g
899	128	8.0	506	1	SHP51_BOVIN	Q46631 bos taurus	972	125.5	7.8	306	2	Q9QYL4_MOUSE	Q9qyl4 mus musculus
900	128	8.0	507	2	Q5K4Q3_PIG	Q5k4q3 sus scrofa	973	125.5	7.8	310	2	Q4V8T3_BRARE	Q4v8t3 brachydanio
901	128	8.0	518	2	Q1RKQ9_DROME	Q1rkq9 drosophila	974	125.5	7.8	340	2	Q9W3N2_DROME	Q9w3n2 drosophila
902	128	8.0	531	2	Q7QEY7_ANOGA	Q7qey7 anopheles g	975	125.5	7.8	341	2	Q61354_MOUSE	Q61354 mus musculus
903	128	8.0	714	2	Q4T313_TETNG	Q4t313 tetraodon n	976	125.5	7.8	341	2	Q1JPK2_BRARE	Q1jpk2 brachydanio
904	128	8.0	773	2	Q32MJ8_HUMAN	Q32mj8 homo sapien	977	125.5	7.8	352	2	Q08266_HUMAN	Q08266 homo sapien
905	128	8.0	869	1	MUSK_HUMAN	Q15146 homo sapien	978	125.5	7.8	352	2	Q15403_HUMAN	Q15403 homo sapien
906	128	8.0	1180	2	Q51S85_9PRIM	Q5is85 saimir bol	979	125.5	7.8	465	2	Q640J0_XENLA	Q640j0 xenopus lae
907	128	8.0	1363	1	VGFR3_MOUSE	P35917 mus musculus	980	125.5	7.8	480	2	Q9PSD1_9PIPI	Q9psd1 xenopus. fi

981	125.5	7.8	510	2	Q801V8 BRARE	Q801V8 brachydanio	1054	123.5	7.7	4560	2	Q161U1_AEDAE	Q161U1 aedes aegyp
982	125.5	7.8	590	2	Q4SPp8_TETNG	Q4SPp8 tetraodon n	1055	123	7.7	302	1	ICOSL_HUMAN	Q75144 homo sapien
983	125.5	7.8	769	2	Q8N15_HUMAN	Q8N15 homo sapien	1056	123	7.7	370	1	Q800Y8 BRARE	Q800Y8 brachydanio
984	125.5	7.8	806	1	Q8FR3_HUMAN	P22607 homo sapien	1057	123	7.7	411	1	Q15228_HUMAN	Q15228 homo sapien
985	125.5	7.8	838	1	Q4SPp3_TETNG	Q4SPp9 tetraodon n	1058	123	7.7	442	1	SIGL6_HUMAN	Q43699 homo sapien
986	125.5	7.8	1028	1	CNTN3_HUMAN	Q9P232 homo sapien	1059	123	7.7	462	2	Q6GLT3_XENLA	Q6GLT3 xenopus lae
987	125.5	7.8	1040	2	Q9W675 BRARE	Q9W675 brachydanio	1060	123	7.7	515	1	PVRL1_PIG	Q9J176 sus scrofa
988	125.5	7.8	1140	2	Q372P5_MOUSE	Q372p5 mus musculus	1061	123	7.7	622	2	Q9JKB2_MOUSE	Q9JKB2 mus musculus
989	125.5	7.8	1154	2	Q4SR22_TETNG	Q4SR22 tetraodon n	1062	123	7.7	648	1	MUC18_MOUSE	Q8R2V2 mus musculus
990	125.5	7.8	1242	1	NPHN_MOUSE	Q9SZ87 mus musculus	1063	123	7.7	656	2	Q4SPp7_TETNG	Q4SPp7 tetraodon n
991	125.5	7.8	1256	2	Q9Z5S5_MOUSE	Q9Z5S5 mus musculus	1064	123	7.7	692	2	Q800Y9 BRARE	Q800Y9 brachydanio
992	125.5	7.8	1256	2	Q9ET59_MOUSE	Q9ET59 mus musculus	1065	123	7.7	756	2	Q800Z0 BRARE	Q800Z0 brachydanio
993	125.5	7.8	1256	2	Q9JIX1_MOUSE	Q9JIX1 mus musculus	1066	123	7.7	776	2	Q4RHT1_TETNG	Q4RHT1 tetraodon n
994	125.5	7.8	1445	2	Q63155_RAT	Q63155 rattus norv	1067	123	7.7	820	2	Q53H63_HUMAN	Q53H63 homo sapien
995	125.5	7.8	1447	1	DCC_MOUSE	P70211 mus musculus	1068	123	7.7	903	2	Q29JX6_DROPS	Q29JX6 drosophila
996	125	7.8	219	2	Q8W91_HUMAN	Q8W91 homo sapien	1069	123	7.7	922	2	Q90413_BRARE	Q90413 brachydanio
997	125	7.8	325	2	Q8HW98_MOUSE	Q8HW98 mus musculus	1070	123	7.7	1040	1	CNTN2_HUMAN	Q02246 homo sapien
998	125	7.8	464	2	Q1XD56_MOUSE	Q1XD56 mus musculus	1071	123	7.7	1040	2	Q5T054_HUMAN	Q5T054 homo sapien
999	125	7.8	617	2	Q49AF3_HUMAN	Q49AF3 homo sapien	1072	123	7.7	1051	1	LRIG1_MOUSE	P70193 mus musculus
1000	125	7.8	775	2	Q6PF50_XENLA	Q6PF50 xenopus lae	1073	123	7.7	1250	2	Q8TDY8_HUMAN	Q8TDY8 homo sapien
1001	125	7.8	860	2	Q32S49_MOUSE	Q32S49 mus musculus	1074	123	7.7	1251	2	Q8CHB2_MOUSE	Q8CHB2 mus musculus
1002	125	7.8	868	1	MUSK_MOUSE	Q61006 mus musculus	1075	123	7.7	1723	2	Q16PP3_AEDAE	Q16PP3 aedes aegyp
1003	125	7.8	868	2	Q3ZS50_MOUSE	Q3ZS50 mus musculus	1076	123	7.7	2703	2	Q9SYM1_PROCL	Q9SYM1 procambatus
1004	125	7.8	956	1	MAMC1_HUMAN	Q72553 homo sapien	1077	123	7.7	4824	2	TITIN_DROME	Q9I704 drosophila
1005	125	7.8	1100	1	CNTN5_HUMAN	Q94779 homo sapien	1078	122.5	7.6	18074	1	Q961T8_DROME	Q961T8 drosophila
1006	125	7.8	1180	2	Q5IS40_PANTR	Q5IS40 pan troglod	1079	122.5	7.6	336	2	Q4H1G8_SAMCR	Q4H1G8 samia cynth
1007	125	7.8	1197	1	L1CA1_BRARE	Q90478 brachydanio	1080	122.5	7.6	413	2	Q17HBI_AEDAE	Q17HBI aedes aegyp
1008	125	7.8	2212	2	Q8W9N3_HUMAN	Q8W9N3 homo sapien	1081	122.5	7.6	505	2	Q5W434_BRARE	Q5W434 brachydanio
1009	125	7.8	22017	2	Q7Z246_BRARE	Q7Z246 brachydanio	1082	122.5	7.6	633	2	Q5W433_BRARE	Q5W433 brachydanio
1010	124.5	7.8	290	2	Q5TNT8_ANOGA	Q5TNT8 anophelles g	1083	122.5	7.6	651	2	Q9GKR3_BOVIN	Q9GKR3 bos taurus
1011	124.5	7.8	309	2	Q3TDR5_MOUSE	Q3TDR5 mus musculus	1084	122.5	7.6	739	2	Q4S2G2_TETNG	Q4S2G2 tetraodon n
1012	124.5	7.8	313	2	Q57596_CHICK	Q57596 gallus gall	1085	122.5	7.6	821	2	Q9TX18_CAEBL	Q9TX18 caenorhabdi
1013	124.5	7.8	315	2	Q9DGI5_CHICK	Q9DGI5 gallus gall	1086	122.5	7.6	1156	2	Q676C3_OIKDI	Q676C3 oikopleura
1014	124.5	7.8	344	2	Q93242_CHICK	Q93242 gallus gall	1087	122.5	7.6	1255	2	Q17PE4_AEDAE	Q17PE4 aedes aegyp
1015	124.5	7.8	349	2	Q17524_AEDAE	Q17524 aedes aegyp	1088	122.5	7.6	1746	2	Q8WT19_HUMAN	Q8WT19 homo sapien
1016	124.5	7.8	419	2	Q68CR6_HUMAN	Q68CR6 homo sapien	1089	122.5	7.6	2012	1	DSCAM_HUMAN	Q60469 homo sapien
1017	124.5	7.8	426	1	PSG8_HUMAN	Q9UQ74 homo sapien	1090	122.5	7.6	2013	2	Q8VHZ8_RAT	Q8VHZ8 rattus norv
1018	124.5	7.8	822	2	Q9QV77_9MURI	Q9QV77 rattus sp.	1091	122.5	7.6	2023	2	Q59GH3_HUMAN	Q59GH3 homo sapien
1019	124.5	7.8	1047	2	Q4RGCT_TETNG	Q4RGCT tetraodon n	1092	122	7.6	312	2	Q4SUX1_TETNG	Q4SUX1 tetraodon n
1020	124.5	7.8	1241	1	NPHN_HUMAN	Q60500 homo sapien	1093	122	7.6	332	1	CD22_GORGO	Q9N1E4 gorilla gor
1021	124.5	7.8	1320	1	MYFN_HUMAN	Q86TC9 homo sapien	1094	122	7.6	413	2	Q1EC36_DROME	Q1EC36 drosophila
1022	124.5	7.8	5724	2	Q7PT04_ANOGA	Q7PT04 anophelles g	1095	122	7.6	513	2	Q9DGN4_MOUSE	Q9DGN4 mus musculus
1023	124.5	7.8	8625	2	Q8GGD6_PROCL	Q8GGD6 procambatus	1096	122	7.6	524	2	Q3UM26_MOUSE	Q3UM26 mus musculus
1024	124	7.7	241	2	Q17N41_AEDAE	Q17N41 aedes aegyp	1097	122	7.6	582	2	Q8R4B5_MOUSE	Q8R4B5 mus musculus
1025	124	7.7	253	2	Q9D8H2_MOUSE	Q9D8H2 m adult mal	1098	122	7.6	595	2	Q7Q3K8_ANOGA	Q7Q3K8 anopheles g
1026	124	7.7	258	2	Q8Y334_DROPS	Q8Y334 drosophila	1099	122	7.6	813	1	FGFR2_XENLA	Q7Q364 xenopus lae
1027	124	7.7	585	1	CEA20_HUMAN	Q6UY09 homo sapien	1100	122	7.6	907	2	Q9NEG0_DROME	Q9NEG0 drosophila
1028	124	7.7	879	2	Q59FL9_HUMAN	Q59FL9 homo sapien	1101	122	7.6	915	2	Q8R4B3_MOUSE	Q8R4B3 mus musculus
1029	124	7.7	1028	1	CNTN3_RAT	Q62682 rattus norv	1102	122	7.6	1066	2	Q8MSR5_DROME	Q8MSR5 drosophila
1030	124	7.7	1054	1	LRIG2_MOUSE	Q52KR2 mus musculus	1103	122	7.6	1166	2	Q9QV4_9MURI	Q9QV4 rattus sp.
1031	124	7.7	1069	2	Q2EY13_BRARE	Q2EY13 brachydanio	1104	122	7.6	1252	2	Q9JIX2_RAT	Q9JIX2 rattus norv
1032	124	7.7	1284	1	NRCAM_CHICK	P35331 gallus gall	1105	122	7.6	1288	2	Q624K5_CAEBR	Q624K5 caenorhabdi
1033	124	7.7	1285	2	Q1EN18_CAEBL	Q1EN18 caenorhabdi	1106	122	7.6	1302	1	VGPR2_BRARE	Q8AXB3 brachydanio
1034	124	7.7	1443	2	Q8MTB2_DROME	Q8MTB2 drosophila	1107	122	7.6	3215	2	Q8IRV7_DROME	Q8IRV7 drosophila
1035	124	7.7	1765	2	Q9VS30_DROME	Q9VS30 drosophila	1108	122	7.6	4117	2	Q8IRV9_DROSOPHILA	Q8IRV9 drosophila
1036	124	7.7	1770	2	Q9VS28_DROME	Q9VS28 drosophila	1109	122	7.6	4179	2	Q9W4Y4_DROME	Q9W4Y4 drosophila
1037	124	7.7	2053	1	DSC11_HUMAN	Q9VS29 drosophila	1110	122	7.6	4223	2	Q8MEN3_DROME	Q8MEN3 drosophila
1038	124	7.7	3259	1	SPFG_RAT	Q8TD84 homo sapien	1111	122	7.6	4228	2	Q8IRV8_DROME	Q8IRV8 drosophila
1039	124	7.7	8402	2	Q4RE89_TETNG	Q4RE89 tetraodon n	1112	122	7.6	4629	2	Q9W4Y3_DROME	Q9W4Y3 drosophila
1040	123.5	7.7	299	1	CD80_RABIT	P42070 oryctolagus	1113	122	7.6	5516	2	Q7Z248_BRARE	Q7Z248 brachydanio
1041	123.5	7.7	307	2	Q3U4B5_MOUSE	Q3U4B5 mus musculus	1114	121.5	7.6	304	2	Q9TOX1_CANFA	Q9TOX1 canis famil
1042	123.5	7.7	317	2	QSTQN9_ANOGA	QSTQN9 anophelles g	1115	121.5	7.6	332	1	PSG11_HUMAN	Q8UQ72 homo sapien
1043	123.5	7.7	419	1	PSG1_HUMAN	P11464 homo sapien	1116	121.5	7.6	338	2	Q7Z3W6_HUMAN	Q7Z3W6 homo sapien
1044	123.5	7.7	426	2	Q61CR4_HUMAN	Q61CR4 homo sapien	1117	121.5	7.6	338	2	Q5R7T4_PONPY	Q5R7T4 pongo pygma
1045	123.5	7.7	437	2	Q86YV1_HUMAN	Q86YV1 homo sapien	1118	121.5	7.6	348	2	Q16M91_AEDAE	Q16M91 aedes aegyp
1046	123.5	7.7	440	2	Q6ZMD4_HUMAN	Q6ZMD4 homo sapien	1119	121.5	7.6	424	1	PSG10_HUMAN	Q15235 homo sapien
1047	123.5	7.7	582	2	Q9SN25_BOVIN	Q9SN25 bos taurus	1120	121.5	7.6	428	1	PSG3_HUMAN	Q16557 homo sapien
1048	123.5	7.7	606	2	Q4T4K0_TETNG	Q4T4K0 tetraodon n	1121	121.5	7.6	435	1	PSG6_HUMAN	Q10889 homo sapien
1049	123.5	7.7	766	2	Q7Q0S7_ANOGA	Q7Q0S7 anophelles g	1122	121.5	7.6	602	2	Q52NV2_RAT	Q52NV2 rattus norv
1050	123.5	7.7	1026	1	CNTN4_RAT	Q62845 rattus norv	1123	121.5	7.6	775	2	Q97754_RABIT	Q97754 oryctolagus
1051	123.5	7.7	1319	2	Q4T8B2_TETNG	Q4T8B2 tetraodon n	1124	121.5	7.6	785	2	Q1KHV5_HUMAN	Q1KHV5 homo sapien
1052	123.5	7.7	1409	2	Q617L8_CAEBR	Q617L8 caenorhabdi	1125	121.5	7.6	898	1	PAS2_SCHAM	P22648 schistocerc
1053	123.5	7.7	3158	2	Q4TAD4_TETNG	Q4TAD4 tetraodon n	1126	121.5	7.6	987	2	Q7YZM8_CAEBL	Q7YZM8 caenorhabdi

1127	121.5	7.6	1024	2	Q1HTP2_HAPBU	Q1htp2 haplochromi	1200	7.5	1014	2	Q8NFA6_HUMAN	Q8nfa6 homo sapien
1128	121.5	7.6	1379	2	Q5XNV9_PETWA	Q5xnv9 petromyzon	1201	7.5	1168	2	Q5U3B1_BRARE	Q5u3b1 brachydanio
1129	121.5	7.6	1415	2	Q5XNV8_PETWA	Q5xnv8 petromyzon	1202	7.5	1190	2	Q3S3D8_XENBO	Q3s3d8 xenopus bor
1130	121.5	7.6	2007	2	Q17A19_AEDAE	Q17a19 aedes aegyp	1203	7.5	1205	2	Q8BUJ0_MOUSE	Q8bujo mus musculus
1131	121.5	7.6	2013	2	Q9ERC8_MOUSE	Q9erc8 mus musculus	1204	7.5	1327	2	Q8QHL3_CHICK	Q8qhl3 gallus gall
1132	121.5	7.6	4816	2	Q8T103_BOMWO	Q8t103 bombyx mori	1205	7.5	1332	2	Q9VOW7_DROME	Q9vow7 drosophila
1133	121	7.5	182	2	Q15402_HUMAN	Q15402 homo sapien	1206	7.5	1332	2	Q9BN17_DROME	Q9bn17 drosophila
1134	121	7.5	265	2	Q296A3_DROPS	Q296a3 drosophila	1207	7.5	1725	2	Q7Q916_ANOGA	Q7q916 anopheles g
1135	121	7.5	294	2	Q8BH36_MESAU	Q8bh36 mesocricetu	1208	7.5	4779	2	Q17AE9_AEDAE	Q17aeb9 aedes aegyp
1136	121	7.5	316	2	Q8WUN1_HUMAN	Q8wun1 homo sapien	1209	7.5	9369	2	Q4T444_TETNG	Q4t444 tetraodon n
1137	121	7.5	318	2	Q90293_BRARE	Q90293 brachydanio	1210	119.5	282	2	Q9H6B2_HUMAN	Q9h6b2 homo sapien
1138	121	7.5	319	2	Q8MT24_DROME	Q8mt24 drosophila	1211	119.5	282	2	Q13984_HUMAN	Q13984 homo sapien
1139	121	7.5	328	2	Q8UUV6_BRARE	Q8uuv6 brachydanio	1212	119.5	345	1	OPCM_RAT	P32736 rattus norv
1140	121	7.5	337	2	Q3TYL3_MOUSE	Q3tyl3 mus musculus	1213	119.5	382	2	Q17NM7_AEDAE	Q17nw7 aedes aegyp
1141	121	7.5	337	2	Q6DFY2_MOUSE	Q6dfy2 mus musculus	1214	119.5	386	2	Q4S1B2_TETNG	Q4s1b2 tetraodon n
1142	121	7.5	360	2	Q61565_MOUSE	Q61565 mus musculus	1215	119.5	467	2	Q17NM8_AEDAE	Q17nw8 aedes aegyp
1143	121	7.5	361	2	Q9QW79_9MURI	Q9qw79 mus sp. fib	1216	119.5	507	2	Q3UQ26_MOUSE	Q3uq26 mus musculus
1144	121	7.5	422	2	Q96PJ3_HUMAN	Q96pj3 homo sapien	1217	119.5	509	1	SHPS1_RAT	P97710 r tyrosine-
1145	121	7.5	515	2	Q96PJ5_HUMAN	Q96pj5 homo sapien	1218	7.4	513	2	Q499T3_RAT	Q499t3 rattus norv
1146	121	7.5	515	2	Q9GRE0_HUMAN	Q9gre0 homo sapien	1219	119.5	543	2	Q62218_CAEBR	Q62218 caenorhabdi
1147	121	7.5	557	2	Q4RB52_TETNG	Q4rb52 tetraodon n	1220	119.5	622	2	Q9ESS5_MOUSE	Q9ess5 mus musculus
1148	121	7.5	640	2	Q8BSM2_MOUSE	Q8bsm2 mus musculus	1221	119.5	622	2	Q9R069_MOUSE	Q9r069 mus musculus
1149	121	7.5	733	2	Q8SQ83_TRIVU	Q8sq83 trichosurus	1222	119.5	704	2	Q307W2_FELCA	Q307w2 felis silve
1150	121	7.5	820	2	Q8C1M9_MOUSE	Q8c1m9 mus musculus	1223	119.5	736	2	Q8MYS2_DROME	Q8mys2 drosophila
1151	121	7.5	867	2	Q59DZ1_DROME	Q59dz1 drosophila	1224	119.5	739	1	VCAM1_CANFA	Q28260 canis famli
1152	121	7.5	1018	1	CNTN1_BOVIN	Q28106 bos taurus	1225	7.4	771	2	Q4KM07_HUMAN	Q4kmq7 homo sapien
1153	121	7.5	1040	2	Q5RDT8_PONPY	Q5rdt8 pongo pygma	1226	119.5	774	2	Q9V930_DROME	Q9v930 drosophila
1154	121	7.5	1124	2	Q6PEL5_MOUSE	Q6pel5 mus musculus	1227	119.5	907	2	Q98850_CARAU	Q98850 carassius a
1155	121	7.5	1171	2	Q86TA8_HUMAN	Q86ta8 homo sapien	1228	119.5	1134	2	Q71B05_BRARE	Q71b05 brachydanio
1156	121	7.5	1234	1	NPHN_RAT	Q3t113 bos taurus	1229	119.5	1304	1	NRCAM_HUMAN	Q28823 homo sapien
1157	120.5	7.5	261	1	TMIGD_BOVIN	Q73716 grus americ	1230	119.5	1377	1	NEOL_RAT	P97603 rattus norv
1158	120.5	7.5	280	2	Q73716_GRUAM	Q73716 grus americ	1231	119.5	1639	2	Q3Y5G6_TRICA	Q3y5g6 tribolium c
1159	120.5	7.5	285	2	Q72V30_XENLA	Q72v30 xenopus lae	1232	119.5	4785	2	Q2LYU8_DROPS	Q2lyu8 drosophila
1160	120.5	7.5	327	1	MOX2R_RAT	Q9e580 rattus norv	1233	119	177	2	Q6NUR8_HUMAN	Q6nur8 homo sapien
1161	120.5	7.5	341	2	Q8JTX8_LSDV	Q8jtx8 lumpy skin	1234	119	211	2	Q7PUC4_ANOGA	Q7puc4 anopheles g
1162	120.5	7.5	362	2	Q9JHQ1_RAT	Q9jhq1 rattus norv	1235	119	222	2	Q29LN2_DROPS	Q29ln2 drosophila
1163	120.5	7.5	446	2	Q63236_RAT	Q63236 rattus norv	1236	119	231	2	Q3USC2_MOUSE	Q3usc2 m 10 days n
1164	120.5	7.5	446	2	Q63237_RAT	Q63237 rattus norv	1237	119	306	2	Q5HZT7_XENTR	Q5hzt7 xenopus tro
1165	120.5	7.5	466	2	Q4VMT2_9PIPI	Q4vmt2 xenopus sp.	1238	119	310	1	FCG2B_HUMAN	P31994 homo sapien
1166	120.5	7.5	678	2	Q5XU11_SHEEP	Q5xui1 ovig aries	1239	119	323	1	FCG2C_HUMAN	P31995 homo sapien
1167	120.5	7.5	760	2	Q17OK8_AEDAE	Q17ok8 aedes aegyp	1240	119	342	2	Q5JXA9_HUMAN	Q5jxa9 homo sapien
1168	120.5	7.5	821	1	FGFR2_HUMAN	P21802 homo sapien	1241	119	454	1	BTNL2_RAT	Q6mg97 rattus norv
1169	120.5	7.5	1026	1	CNTN4_HUMAN	Q8iww2 homo sapien	1242	119	481	2	Q6OND3_CAEBR	Q6ond3 caenorhabdi
1170	120.5	7.5	1049	2	Q4SOF2_TETNG	Q4sof2 tetraodon n	1243	119	515	1	PVRL1_MOUSE	Q91kf5 mus musculus
1171	120.5	7.5	1276	2	Q9QX22_BRARE	Q9qx22 brachydanio	1244	119	515	2	Q6P9M5_MOUSE	Q6p9m5 mus musculus
1172	120.5	7.5	1421	2	Q49BB0_BRARE	Q49bb0 brachydanio	1245	119	627	2	Q5RDU0_PONPY	Q5rdu0 pongo pygma
1173	120.5	7.5	1505	2	Q17F56_AEDAE	Q17f56 aedes aegyp	1246	119	765	2	Q9BKQ1_APLCA	Q9bkq1 aplysia cal
1174	120.5	7.5	1944	2	Q4SPG3_TETNG	Q4spg3 tetraodon n	1247	119	765	2	Q9TWA4_APLCA	Q9twa4 aplysia cal
1175	120.5	7.5	4203	2	Q965G2_CABEL	Q965g2 caenorhabdi	1248	119	812	2	Q9BKQ0_APLCA	Q9bkq0 aplysia cal
1176	120.5	7.5	4219	2	Q9NL87_CABEL	Q9nl87 caenorhabdi	1249	119	812	2	Q9TWA5_APLCA	Q9twa5 aplysia cal
1177	120.5	7.5	4250	2	Q5PY59_CABEL	Q5py59 caenorhabdi	1250	119	816	2	Q91285_PLEWA	Q91285 pleurodeles
1178	120.5	7.5	4369	2	Q8MXD7_CABEL	Q8mxd7 caenorhabdi	1251	119	862	2	Q4SST3_TETNG	Q4sst3 tetraodon n
1179	120.5	7.5	4889	2	Q9TXK2_CABEL	Q9txk2 caenorhabdi	1252	119	865	2	Q68DA2_HUMAN	Q68da2 homo sapien
1180	120	7.5	200	2	Q4RRS2_TETNG	Q4rrs2 tetraodon n	1253	119	932	2	Q9BKP9_APLCA	Q9bkp9 aplysia cal
1181	120	7.5	238	2	Q20339_CABEL	Q20339 caenorhabdi	1254	119	932	2	Q9TWA6_APLCA	Q9twa6 aplysia cal
1182	120	7.5	298	2	Q81NK5_DROME	Q81nk5 drosophila	1255	119	961	1	ROBO4_RAT	Q8ow87 rattus norv
1183	120	7.5	357	2	Q18872_PIG	Q18872 sus scrofa	1256	119	1007	1	ROBO4_HUMAN	Q8ow87 homo sapien
1184	120	7.5	376	2	Q9QW78_9MURI	Q9qw78 mus sp. fib	1257	119	1018	1	CNTN1_HUMAN	Q12860 homo sapien
1185	120	7.5	399	1	VSIG4_HUMAN	Q9y279 homo sapien	1258	119	1301	2	Q29M24_DROPS	Q29m24 drosophila
1186	120	7.5	459	2	Q86X91_HUMAN	Q86x91 homo sapien	1259	119	1441	2	Q3S3D7_XENBO	Q3s3d7 xenopus bor
1187	120	7.5	483	2	Q7SX76_BRARE	Q7sx76 brachydanio	1260	119	74	2	Q17HV9_AEDAE	Q17hv9 aedes aegyp
1188	120	7.5	524	1	BTIA1_MOUSE	Q62556 mus musculus	1261	119	74	2	Q7KQP7_DROME	Q7kqp7 drosophila
1189	120	7.5	534	2	Q5SQU6_MOUSE	Q5sasu6 mus musculus	1262	119	74	2	Q801W8_BRARE	Q801w8 brachydanio
1190	120	7.5	677	2	Q8QHL2_CHICK	Q8qhl2 gallus gall	1263	118.5	230	2	Q9N164_PAPHA	Q9n164 papio hamad
1191	120	7.5	773	2	Q59FV9_HUMAN	Q59fv9 homo sapien	1264	118.5	286	2	Q2TA28_BOVIN	Q2ta28 bos taurus
1192	120	7.5	814	2	Q59H40_HUMAN	Q59h40 homo sapien	1265	118.5	294	2	Q17NU7_AEDAE	Q17nu7 aedes aegyp
1193	120	7.5	820	2	Q5R8Q3_PONPY	Q5r8q3 pongo pygma	1266	118.5	294	2	Q8SPW3_MACFA	Q8spw3 macaca fasc
1194	120	7.5	822	1	FGFR1_HUMAN	P11362 homo sapien	1267	118.5	308	2	Q9UFM8_HUMAN	Q9ufm8 homo sapien
1195	120	7.5	822	1	FGFR1_MOUSE	P16092 mus musculus	1268	118.5	317	1	FCG2A_HUMAN	P12318 homo sapien
1196	120	7.5	822	1	FGFR1_RAT	Q04589 rattus norv	1269	118.5	319	2	Q5ISM6_MACFA	Q5ism6 macaca fasc
1197	120	7.5	822	2	Q60818_MOUSE	Q60818 mus musculus	1270	118.5	410	2	Q4FAT1_BOMWO	Q4fat1 bombyx mori
1198	120	7.5	888	2	Q4VBK2_BRARE	Q4vbk2 brachydanio	1271	118.5	432	2	Q52NV1_RAT	Q52nvl rattus norv
1199	120	7.5	939	2	Q9VH85_DROME	Q9vh85 drosophila	1272	118.5	477	2	Q5EAJ2_FUGRU	Q5eaj2 fugu rubrip

1273	118.5	7.4	478	2	Q4RVM0	TETNG	Q4RVM0	tetraodon n	1346	117	7.3	316	1	FCG2A_PANTR	Q8spv8 pan troglod
1274	118.5	7.4	534	2	Q25403	LYMST	Q25403	lymaea sta	1347	117	7.3	330	1	CD22_PONPY	Q9n163 pongo pygma
1275	118.5	7.4	650	2	Q99K86	MOUSE	Q99K86	mus musculus	1348	117	7.3	351	2	Q8JFU3_BRARE	Q8jfu3 brachydanio
1276	118.5	7.4	739	1	VCAM1_HUMAN		P13320	homo sapien	1349	117	7.3	351	2	Q7SY58_BRARE	Q7sy58 brachydanio
1277	118.5	7.4	739	2	Q35FL7_HUMAN		Q53f17	homo sapien	1350	117	7.3	484	2	Q99JQ8_MOUSE	Q99jq8 mus musculus
1278	118.5	7.4	763	2	Q7PUH1_ANOPHELES	g	Q7puh1	anopheles g	1351	117	7.3	501	2	Q6Q147_BOVIN	Q6q147 bos taurus
1279	118.5	7.4	772	2	Q49AK4_HUMAN		Q49ak4	homo sapien	1352	117	7.3	513	1	SHFS1_MOUSE	P97797 m tyrosine-
1280	118.5	7.4	829	2	Q4RIG0_TETNG		Q4rig0	tetraodon n	1353	117	7.3	538	2	Q9QYQ7_MOUSE	Q9qyq7 mus musculus
1281	118.5	7.4	877	2	Q9GSH3_HALOCYTHIA		Q9gsh3	halocynthia	1354	117	7.3	588	2	Q6MG92_RAT	Q6mg92 rattus norv
1282	118.5	7.4	1065	2	Q4RH24_TETNG		Q4rh24	tetraodon n	1355	117	7.3	669	2	Q6B515_POEGU	Q6b515 poephila gu
1283	118.5	7.4	1098	2	Q8RG33_BRARE		Q59j3	brachydanio	1356	117	7.3	686	2	Q7PQM9_ANOGA	Q7pqm9 anopheles g
1284	118.5	7.4	1119	1	LRIG3_HUMAN		Q6uxm1	homo sapien	1357	117	7.3	949	1	MAMC1_RAT	P60756 rattus norv
1285	118.5	7.4	1280	2	Q9EPX2_MOUSE		Q9epx2	mus musculus	1358	117	7.3	986	2	Q8UVR9_FUGRU	Q8uvr9 fugu rubrip
1286	118.5	7.4	1443	1	SN01_CHICK		Q90610	gallus gall	1359	117	7.3	1029	2	Q596X0_CARAU	Q596x0 carassius a
1287	118.5	7.4	1694	1	SN_MOUSE		Q62230	mus musculus	1360	117	7.3	1033	2	Q4SBZ7_TETNG	Q4sbz7 tetraodon n
1288	118.5	7.4	2007	2	Q4SM88_TETNG		Q4sm88	tetraodon n	1361	117	7.3	1040	1	CNTN2_RAT	P22063 rattus norv
1289	118.5	7.4	6658	2	Q76281_DROME		Q76281	drosophila	1362	117	7.3	1193	2	Q9VQW1_DROME	Q9vqw1 drosophila
1290	118.5	7.4	282	2	Q501W4_RAT		Q501w4	rattus norv	1363	117	7.3	1596	2	Q9HCL6_HUMAN	Q9hcl6 homo sapien
1291	118.5	7.4	289	2	Q5JXB0_HUMAN		Q5jxb0	homo sapien	1364	116.5	7.3	220	2	Q7QHC6_ANOGA	Q7qhc6 anopheles g
1292	118.5	7.4	316	2	Q8W64_HUMAN		Q8w64	homo sapien	1365	116.5	7.3	236	2	Q15461_HUMAN	Q15461 homo sapien
1293	118.5	7.4	317	2	Q86915_9POXV		Q86915	sheepox vi	1366	116.5	7.3	315	2	Q563H0_ONCMY	Q563h0 oncorhynch
1294	118.5	7.4	326	2	Q9UPK8_HUMAN		Q9upk8	homo sapien	1367	116.5	7.3	333	2	Q75238_HUMAN	Q75238 homo sapien
1295	118.5	7.4	328	2	Q8UJ20_LSDV		Q8ju20	lumpy skin	1368	116.5	7.3	337	2	Q9IAZ4_9PERC	Q9ia44 spherooides
1296	118.5	7.4	337	2	Q5D095_MOUSE		Q5d095	mus musculus	1369	116.5	7.3	345	1	OPCM_HUMAN	P11834 bos taurus
1297	118.5	7.4	341	2	Q91M21_LSDV		Q91m21	lumpy skin	1370	116.5	7.3	345	1	OPCM_HUMAN	Q14982 homo sapien
1298	118.5	7.4	422	2	Q8WR61_LYMDI		Q8wr61	lymantria d	1371	116.5	7.3	345	1	OPCM_PANTR	Q15161 pan troglod
1299	118.5	7.4	429	2	Q60F95_HUMAN		Q60f95	homo sapien	1372	116.5	7.3	345	1	OPCM_PANTR	Q17rn7 homo sapien
1300	118.5	7.4	567	1	LRKL1_MOUSE		P14719	mus musculus	1373	116.5	7.3	377	2	Q8OV04_MOUSE	Q8ov04 mus musculus
1301	118.5	7.4	584	2	Q93Y8_HUMAN		Q93y8	homo sapien	1374	116.5	7.3	402	2	Q15227_HUMAN	Q15227 homo sapien
1302	118.5	7.4	602	2	Q9VFD9_DROME		Q9vfd9	drosophila	1375	116.5	7.3	416	2	Q96360_HYPCU	Q96360 hypanthia
1303	118.5	7.4	941	2	Q5J1R9_BRARE		Q5j1r9	brachydanio	1376	116.5	7.3	426	1	PSG9_HUMAN	Q90887 homo sapien
1304	118.5	7.4	949	1	MAMC1_MOUSE		P60755	mus musculus	1377	116.5	7.3	426	1	Q6LEU7_HUMAN	Q6leu7 homo sapien
1305	118.5	7.4	1025	2	Q3UV20_MOUSE		Q3uv20	mus musculus	1378	116.5	7.3	513	1	BT3A1_HUMAN	Q00481 homo sapien
1306	118.5	7.4	1032	1	CNT1A_BRARE		Q8axz4	brachydanio	1379	116.5	7.3	536	2	Q8BJE2_MOUSE	Q8bje2 mus musculus
1307	118.5	7.4	1148	2	Q86T39_HUMAN		Q86t39	homo sapien	1380	116.5	7.3	541	2	Q95XJ7_CABER	Q95xj7 caenorhabdi
1308	118.5	7.4	1154	2	Q9QV33_RAT		Q9qv33	rattus sp.	1381	116.5	7.3	646	1	MUC18_HUMAN	P43121 h cell surf
1309	118.5	7.4	1194	2	Q6PW33_RAT		Q6pw33	rattus norv	1382	116.5	7.3	699	2	Q61V11_CABER	Q61v11 caenorhabdi
1310	118.5	7.4	1197	2	Q6PW38_RAT		Q6pw38	rattus norv	1383	116.5	7.3	739	1	VCAM1_RAT	Q29534 rattus norv
1311	118.5	7.4	1198	2	Q6PW33_RAT		Q6pw37	rattus norv	1384	116.5	7.3	739	2	Q5FVS3_RAT	Q5fvs3 rattus norv
1312	118.5	7.4	1206	2	Q6PW36_RAT		Q6pw36	rattus norv	1385	116.5	7.3	764	1	PIGR_HUMAN	P01833 homo sapien
1313	118.5	7.4	1209	2	Q6PW39_RAT		Q6pw39	rattus norv	1386	116.5	7.3	764	2	Q68D81_HUMAN	Q68d81 homo sapien
1314	118.5	7.4	1214	1	NRCAM_RAT		P97686	rattus norv	1387	116.5	7.3	856	2	Q1JUB8_BOMMO	Q1jub8 bombyx mori
1315	118.5	7.4	1256	1	NRCAM_MOUSE		Q810u4	mus musculus	1388	116.5	7.3	998	2	Q9W4Y6_DROME	Q9w4y6 drosophila
1316	118.5	7.4	1299	2	Q8PW31_RAT		Q6pw34	rattus norv	1389	116.5	7.3	998	2	Q95R27_DROME	Q95r27 drosophila
1317	118.5	7.4	6875	2	Q28733_RABIT		Q28733	oryctolagus	1390	116.5	7.3	1120	2	Q17RR7_HUMAN	Q17rr7 homo sapien
1318	118.5	7.4	8647	2	Q7KQP5_DROME		Q7kqp5	drosophila	1391	116.5	7.3	1123	2	Q569K7_HUMAN	Q569k7 homo sapien
1319	118.5	7.4	8648	2	Q7KQP6_DROME		Q7kqp6	drosophila	1392	116.5	7.3	1141	1	MYPC1_HUMAN	Q90872 homo sapien
1320	118.5	7.4	8943	2	Q9V4F7_DROME		Q9v4f7	drosophila	1393	116.5	7.3	1148	2	Q8N3L2_HUMAN	Q8n3l2 homo sapien
1321	117.5	7.3	173	2	Q7PSS8_ANOGA		Q7ps88	anopheles g	1394	116.5	7.3	1148	2	Q8N3R4_HUMAN	Q8n3r4 homo sapien
1322	117.5	7.3	265	2	Q61XU3_CABER		Q61xu3	caenorhabdi	1395	116.5	7.3	1171	2	Q86T48_HUMAN	Q86t48 homo sapien
1323	117.5	7.3	278	2	Q99232_MOUSE		Q99232	mus musculus	1396	116.5	7.3	1171	2	Q86TC8_HUMAN	Q86tc8 homo sapien
1324	117.5	7.3	323	2	Q32QB1_ONCMY		Q32qb1	oncorhynch	1397	116.5	7.3	1266	1	NGCA_CHICK	Q3696 gallus gall
1325	117.5	7.3	323	2	Q563Y2_ONCMY		Q563y2	oncorhynch	1398	116.5	7.3	1403	2	Q4RWS0_TETNG	Q4rws0 tetraodon n
1326	117.5	7.3	328	2	Q29124_DROPS		Q29124	drosophila	1399	116.5	7.3	1403	2	Q29M21_DROPS	Q29m21 drosophila
1327	117.5	7.3	332	2	Q8TA95_HUMAN		Q8ta95	homo sapien	1400	116.5	7.3	1879	2	Q7Q0X2_ANOGA	Q7q0x2 anopheles g
1328	117.5	7.3	336	2	Q5ISA8_9PRIM		Q5isa8	saimiri bol	1401	116.5	7.3	1995	2	Q5TNW7_ANOGA	Q5tnw7 anopheles g
1329	117.5	7.3	391	2	Q76CT6_MOUSE		Q76ct6	mus musculus	1402	116.5	7.3	1995	2	Q61RS53_CABER	Q61rs53 caenorhabdi
1330	117.5	7.3	400	2	Q4T054_TETNG		Q4t054	tetraodon n	1403	116	7.2	4194	2	Q61RS53_CABER	Q61rs53 caenorhabdi
1331	117.5	7.3	400	2	Q71B6_AEDAE		Q71b6	aedes aegyp	1404	116	7.2	182	2	Q51108_HUMAN	Q51108 homo sapien
1332	117.5	7.3	410	2	Q1JPT9_BRARE		Q1jpt9	brachydanio	1405	116	7.2	265	2	Q4SCU0_TETNG	Q4scu0 tetraodon n
1333	117.5	7.3	441	2	Q8C138_MOUSE		Q8c139	mus musculus	1406	116	7.2	310	2	Q8SPW4_MACFA	Q8spw4 macaca fasc
1334	117.5	7.3	495	2	Q4TAJ7_TETNG		Q4taj7	tetraodon n	1407	116	7.2	332	2	Q6UXG3_HUMAN	Q6uxg3 homo sapien
1335	117.5	7.3	782	2	Q9T233_RABIT		Q9t233	oryctolagus	1408	116	7.2	335	1	PSG5_HUMAN	Q15238 homo sapien
1336	117.5	7.3	800	2	Q918X3_BRARE		Q918x3	brachydanio	1409	116	7.2	345	2	Q6GM08_XENIA	Q6gm08 xenopus lae
1337	117.5	7.3	819	1	FGFR1_CHICK		P21804	gallus gall	1410	116	7.2	457	2	Q96OD1_DROME	Q96od1 drosophila
1338	117.5	7.3	879	2	Q8VI95_RAT		Q8vi99	rattus norv	1411	116	7.2	595	2	Q5W431_FUGRU	Q5w431 fugu rubrip
1339	117.5	7.3	888	2	Q8VIA0_RAT		Q8via0	rattus norv	1412	116	7.2	630	2	Q5W435_FUGRU	Q5w435 fugu rubrip
1340	117.5	7.3	939	2	Q9VB35_DROME		Q9vb35	drosophila	1413	116	7.2	648	2	Q5W435_FUGRU	Q5w435 fugu rubrip
1341	117.5	7.3	939	2	Q967X6_DROME		Q967x6	drosophila	1414	116	7.2	707	2	Q5BU23_MOUSE	Q5bu23 mus musculus
1342	117.5	7.3	1005	2	P79921_XENIA		P79921	xenopus lae	1415	116	7.2	737	2	Q1MT46_BRARE	Q1mt46 brachydanio
1343	117.5	7.3	1238	2	Q4S5S6_TETNG		Q4s5s6	tetraodon n	1416	116	7.2	743	2	Q17AC3_AEDAE	Q17ac3 aedes aegyp
1344	117	7.3	279	2	Q563G9_ONCMY		Q563g9	oncorhynch	1417	116	7.2	779	2	Q8N116_HUMAN	Q8n116 homo sapien
1345	117	7.3	293	2	Q563H1_ONCMY		Q563h1	oncorhynch	1418	116	7.2	851	2	Q4STG7_TETNG	Q4stg7 tetraodon n
														Q7Q0S6_ANOGA	Q7q0s6 anopheles g

1419	116	7.2	924	2	Q17HV8	AEADAE	Q17hv8 aedes aegypti
1420	116	7.2	1012	1	ROBO4	MOUSE	Q8C310 mus musculus
1421	116	7.2	1033	2	Q17G69	AEADAE	Q17g69 aedes aegypti
1422	116	7.2	1427	2	Q9VZT8	DROME	Q8T96 drosophila
1423	116	7.2	1461	2	Q8T9F6	DROME	Q8t9f6 drosophila
1424	116	7.2	1509	2	Q9VL08	DROME	Q9vlg8 drosophila
1425	116	7.2	2193	1	SK1	MOUSE	Q3uh53 mus musculus
1426	116	7.2	2558	2	Q6NR91	DROME	Q6nr91 drosophila
1427	116	7.2	2828	2	Q9NR99	HUMAN	Q9nr99 homo sapien
1428	116	7.2	3652	2	Q16PL9	AEADAE	Q16pl9 aedes aegypti
1429	115.5	7.2	180	2	Q15107	HUMAN	Q15107 homo sapien
1430	115.5	7.2	187	2	Q6P097	HUMAN	Q6p097 homo sapien
1431	115.5	7.2	189	2	Q15106	HUMAN	Q15106 homo sapien
1432	115.5	7.2	288	2	Q28499	MACMU	Q28499 macaca mula
1433	115.5	7.2	296	2	Q8WMZ2	FIG	Q8wmz2 sus scrofa
1434	115.5	7.2	324	2	Q6UPK9	HUMAN	Q6upk9 homo sapien
1435	115.5	7.2	332	2	Q5SP74	BRARE	Q5spt4 brachydanio
1436	115.5	7.2	335	2	Q75237	HUMAN	Q75237 homo sapien
1437	115.5	7.2	398	2	Q5SX11	HUMAN	Q5sx11 homo sapien
1438	115.5	7.2	410	2	Q6R3M0	BOMMO	Q6r3m0 bombyx mori
1439	115.5	7.2	410	2	Q6R319	BOMMA	Q6r319 bombyx mand
1440	115.5	7.2	410	2	Q6R3M2	BOMMO	Q6r3m2 bombyx mori
1441	115.5	7.2	422	2	Q86CV9	HELAM	Q86cy9 helicoverpa
1442	115.5	7.2	452	2	Q4RSY9	MACFA	Q4rsy9 macaca fasc
1443	115.5	7.2	513	2	Q53F15	HUMAN	Q53f15 homo sapien
1444	115.5	7.2	517	1	PVRL1	HUMAN	Q51223 homo sapien
1445	115.5	7.2	517	2	Q2M3D3	HUMAN	Q2m3d3 homo sapien
1446	115.5	7.2	626	2	Q4SM56	TFITNG	Q4sm56 tetraodon n
1447	115.5	7.2	636	2	Q22040	CABEL	Q22040 caenorhabdi
1448	115.5	7.2	731	2	Q8SP16	MACEU	Q8sp16 macropus eu
1449	115.5	7.2	743	2	Q6R6B2	9CAUD	Q6rcb2 vibrio phag
1450	115.5	7.2	755	2	Q8CCF8	MOUSE	Q8ccf8 mus musculus
1451	115.5	7.2	824	2	Q91286	PLEWA	Q91286 pleurodeles
1452	115.5	7.2	879	2	Q6PE80	MOUSE	Q6pe80 mus musculus
1453	115.5	7.2	888	1	UFO	MOUSE	Q00993 mus musculus
1454	115.5	7.2	888	2	Q80YQ3	MOUSE	Q80yq3 mus musculus
1455	115.5	7.2	1032	2	Q16ER1	AEADAE	Q16er1 aedes aegypti
1456	115.5	7.2	1248	2	Q9XT41	CERAE	Q9xt41 cercopithec
1457	115.5	7.2	2325	1	SDK CAEL		Q9nx8 caenorhabdi
1458	115.5	7.2	3317	2	Q7QJK9	ANOGA	Q7qjk9 anopheles g
1459	115	7.2	151	2	Q6JDC3	DISMA	Q6jdc3 dissoctichu
1460	115	7.2	226	2	Q8N440	HUMAN	Q8n440 homo sapien
1461	115	7.2	287	2	Q4SL89	TFITNG	Q4sl89 tetraodon n
1462	115	7.2	308	2	Q7Q863	ANOGA	Q7q863 anopheles g
1463	115	7.2	326	2	Q8NC17	HUMAN	Q8nc17 homo sapien
1464	115	7.2	344	2	Q6B014	HUMAN	Q6b014 homo sapien
1465	115	7.2	346	2	Q9CT13	MOUSE	Q9ct13 mus musculus
1466	115	7.2	348	1	NEGR1	MOUSE	Q80z24 mus musculus
1467	115	7.2	351	2	Q15225	HUMAN	Q15225 homo sapien
1468	115	7.2	354	1	NEGR1	HUMAN	Q7z3b1 homo sapien
1469	115	7.2	364	2	Q6GNC2	XENLA	Q6gnc2 xenopus lae
1470	115	7.2	509	2	Q6P618	MOUSE	Q6p618 mus musculus
1471	115	7.2	548	2	Q7PMJ7	ANOGA	Q7pmj7 anopheles g
1472	115	7.2	600	2	Q8N7W7	MOUSE	Q8n7w7 homo sapien
1473	115	7.2	602	1	NRG1	CHICK	Q05199 gallus gall
1474	115	7.2	649	2	Q59F24	HUMAN	Q59f24 homo sapien
1475	115	7.2	823	1	CEK3	CHICK	P18461 gallus gall
1476	115	7.2	824	2	Q90749	CHICK	Q90749 gallus gall
1477	115	7.2	912	1	ICAMS	RABIT	Q28730 cryptotagus
1478	115	7.2	917	1	ICAMS	MOUSE	Q60625 mus musculus
1479	115	7.2	917	2	Q3UY19	MOUSE	Q3uy19 mus musculus
1480	115	7.2	1040	1	CNTN2	MOUSE	Q61330 mus musculus
1481	115	7.2	1040	2	Q3UH39	MOUSE	Q3uh39 mus musculus
1482	115	7.2	1255	2	Q7Z329	HUMAN	Q7z329 homo sapien
1483	115	7.2	1255	2	Q7YQL8	PANTR	Q7yql8 pan troglod
1484	115	7.2	1257	1	LICAM	HUMAN	P32004 homo sapien
1485	115	7.2	1298	1	Q6FR3	HUMAN	P35916 homo sapien
1486	115	7.2	1611	2	Q178Q2	AEADAE	Q178q2 aedes aegypti
1487	115	7.2	2322	1	SDK CAEBR		Q60295 caenorhabdi
1488	115	7.2	2323	1	SEEG	HUMAN	Q05772 homo sapien
1489	115	7.2	6692	2	Q20CA1	DROVI	Q20cal drosophila
1490	114.5	7.1	321	2	Q55202	RAT	Q55202 rattus norv
1491	114.5	7.1	341	2	Q61353	MOUSE	Q61353 mus musculus

1492	114.5	7.1	370	2	Q2ABP8	EPTBU	Q2abp8 eptatretus
1493	114.5	7.1	381	2	Q8R4B1	MOUSE	Q8r4b1 mus musculus
1494	114.5	7.1	413	2	Q26438	HYACE	Q26438 hyalophora
1495	114.5	7.1	510	2	Q96NY8	HUMAN	Q96ny8 homo sapien
1496	114.5	7.1	510	2	Q96K15	HUMAN	Q96k15 homo sapien
1497	114.5	7.1	534	2	Q866T2	PANTR	Q866t2 pan troglod
1498	114.5	7.1	534	2	Q2VF33	PANTR	Q2vf33 pan troglod
1499	114.5	7.1	540	2	Q4RR79	TETNG	Q4rr79 tetraodon n
1500	114.5	7.1	562	2	Q6YNR7	BRARE	Q6ynr7 brachydanio

RESULT 1

JAM2_HUMAN

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AC P57087; QXUG56; G6YNC1;

DT 01-DEC-2000, integrated into UniProtKB/Swiss-Prot.

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OC Catarrhini; Hominoidea; Homo.

OX NCBI_Taxid=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA], PROTEIN SEQUENCE OF 29-33, AND TISSUE SPECIFICITY.

RC TISSUE=Vascular endothelial cell;

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1492	114.5	7.1	370	2	Q2ABP8	EPTBU	Q2abp8 eptatretus
1493	114.5	7.1	381	2	Q8R4B1	MOUSE	Q8r4b1 mus musculus
1494	114.5	7.1	413	2	Q26438	HYACE	Q26438 hyalophora
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1496	114.5	7.1	510	2	Q96K15	HUMAN	Q96k15 homo sapien
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1498	114.5	7.1	534	2	Q2VF33	PANTR	Q2vf33 pan troglod
1499	114.5	7.1	540	2	Q4RR79	TETNG	Q4rr79 tetraodon n
1500	114.5	7.1	562	2	Q6YNR7	BRARE	Q6ynr7 brachydanio

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RA Gardiner K., Slavov D., Bechtel L., Davison M.; "Annotation of human chromosome 21 for relevance to Down syndrome: gene structure and expression analysis.";

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1495	114.5	7.1	510	2	Q96NY8	HUMAN	Q96ny8 homo sapien
1496	114.5	7.1	510	2	Q96K15	HUMAN	Q96k15 homo sapien
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1498	114.5	7.1	534	2	Q2VF33	PANTR	Q2vf33 pan troglod
1499	114.5	7.1	540	2	Q4RR79	TETNG	Q4rr79 tetraodon n
1500	114.5	7.1	562	2	Q6YNR7	BRARE	Q6ynr7 brachydanio

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AC P57087; QXUG56; G6YNC1;

DT 01-DEC-2000, integrated into UniProtKB/Swiss-Prot.

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Schaefer C.F.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [6]
 RP PROTEIN SEQUENCE OF 29-43.
 RX PubMed=15340161; DOI=10.1110/ps.04682504;
 RA Zhang Z., Hensel W.J.;
 RT "Signal peptide prediction based on analysis of experimentally
 RT verified cleavage sites.";
 RL Protein Sci. 13:2819-2824(2004).
 [7]
 RP INTERACTION WITH JAM3.
 RX PubMed=11590146; DOI=10.1074/jbc.M105972200;
 RA Arrate M.P., Rodriguez J.M., Tran T.M., Brock T.A., Cunningham S.A.;
 RT "Cloning of human junctional adhesion molecule 3 (JAM3) and its
 RT identification as the JAM2 counter-receptor.";
 RL J. Biol. Chem. 276:45826-45832(2001).
 [8]
 RP REVIEW, AND Nomenclature.
 RX MEDLINE=22695901; PubMed=12810109; DOI=10.1016/S1471-4906(03)00117-0;
 RA Muller W.A.;
 RT "Leukocyte-endothelial-cell interactions in leukocyte transmigration
 RT and the inflammatory response.";
 RL Trends Immunol. 24:327-334(2003).
 [9]
 RP GLYCOSYLATION [LARGE SCALE ANALYSIS] AT ASN-98, AND MASS SPECTROMETRY.
 RX PubMed=16335952; DOI=10.1021/pr0502065;
 RA Liu T., Qian W.-J., Gritsenko M.A., Camp D.G. II, Monroe M.E.,
 RA Moore R.J., Smith R.D.;
 RT "Human plasma N-glycoproteome analysis by immunoaffinity subtraction,
 RT hydrazide chemistry, and mass spectrometry.";
 RL J. Proteome Res. 4:2070-2080(2005).
 CC -!- FUNCTION: May play a role in the processes of lymphocyte homing to
 CC secondary lymphoid organs.
 CC -!- SUBUNIT: Interacts with JAM3.
 CC -!- SUBCELLULAR LOCATION: Cell membrane; cell-cell junction; tight
 CC junction; single-pass type I membrane protein [By similarity].
 CC Localized at tight junctions of both epithelial and endothelial
 CC cells [By similarity].
 CC -!- TISSUE SPECIFICITY: Highest expression in the heart, placenta,
 CC lung, foreskin and lymph node. Prominently expressed on high
 CC endothelial venules, also present on the endothelia of other
 CC vessels. Localized to the intercellular boundaries of high
 CC endothelial cells.
 CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
 CC -!- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)
 CC domain.
 CC -!- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)
 CC domain.
 CC
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 CC -----

DR EMBL; AF255910; AAF81223.1; --; mRNA.
 DR EMBL; AY016009; AAG49022.1; --; mRNA.
 DR EMBL; AY077698; AAL82538.1; --; mRNA.
 DR EMBL; AY358361; AAQ88727.1; --; mRNA.
 DR EMBL; BC017779; AAH17779.1; --; mRNA.
 DR UniGene; Hs.517227; --.
 DR HSP; O88792; LF97; --.
 DR Ensemble; ENSG00000154721; Homo sapiens.
 DR H-InVDB; HIX0016038; --.
 DR HGNC; HGNC:14686; JAM2.
 DR MIM; 606870; gene.
 DR RZPD-ProtExp; IOH12137; --.
 DR RZPD-ProtExp; UI062; --.
 DR GO; GO:0005887; C:integral to plasma membrane; NAS.
 DR GO; GO:0016337; P:cell-cell adhesion; NAS.
 DR H-Gene; H:14686; JAM2.
 DR InterPro; IPR013151; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003599; Ig_sub.
 DR InterPro; IPR003598; Ig_sub2.
 DR InterPro; IPR013106; Ig_V-set.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF07686; V-set; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS0835; IG_LIKE; 2.
 KW Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
 KW Membrane; Signal; Tight junction; Transmembrane.
 FT SIGNAL 1 28
 FT CHAIN 29 298
 FT TOPO_DOM 29 238
 FT TRANSMEM 239 259
 FT TOPO_DOM 260 298
 FT DOMAIN 32 127
 FT DOMAIN 134 238
 FT CARBOHYD 98 98
 FT CARBOHYD 187 187
 FT CARBOHYD 236 236
 FT DISULFID 50 109
 FT DISULFID 155 214
 FT CONFLICT 270 298
 FT CONFLICT 289 298
 SQ SEQUENCE 298 AA; 33207 MW; CA78E518E22DCAEE CRC64;
 Query Match 91.9%; Score 1475; DB 1; Length 298;
 Best Local Similarity 100.0%; Pred. No. 1.8e-113; Indels 0; Gaps 0;
 Matches 288; Conservative 0; Mismatches 0;
 QY 1 MARRSHRLLLRLRYLVVALGYHKAQYGFSAKDDQVVTAVYQEAIALACKTPKKTSSR 60
 DB 1 MARRSHRLLLRLRYLVVALGYHKAQYGFSAKDDQVVTAVYQEAIALACKTPKKTSSR 60
 QY 61 LEWKKLGRSVFVYQQTLOGDFKRAEMIDFNIRIKNVTSDAGKTRCEVSAPEQCN 120
 DB 61 LEWKKLGRSVFVYQQTLOGDFKRAEMIDFNIRIKNVTSDAGKTRCEVSAPEQCN 120
 QY 121 LEEDTVTLVLVAPVPSCEVPSALSGTVVELRCQDKEGNPAPEYTFWKDGIENPR 180
 DB 121 LEEDTVTLVLVAPVPSCEVPSALSGTVVELRCQDKEGNPAPEYTFWKDGIENPR 180
 QY 181 LGSQSTNSSTYMTNKTGTLOFTVSKLDTGEYSCEARNVGYRRCPCRMQVDDNLISGI 240
 DB 181 LGSQSTNSSTYMTNKTGTLOFTVSKLDTGEYSCEARNVGYRRCPCRMQVDDNLISGI 240
 QY 241 IAAVVVALVISVGLGVCAQKGYFSKETSFKSNSSSKATTMSN 288
 DB 241 IAAVVVALVISVGLGVCAQKGYFSKETSFKSNSSSKATTMSN 288
 RESULT 2
 Q3MHC0 RAT PRELIMINARY; PRT; 298 AA.
 ID Q3MHC0_RAT

RT "Analysis of the mouse transcriptome based on functional annotation of
 RL 60,770 full-length cDNAs.";
 RN Nature 420:563-573(2002).

NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Schriml L.M., Szaubli F., Suzuki R., Nikaido I., Pesole G., Quackenbush J.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).

NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RL prepare full-length cDNA libraries for rapid discovery of new genes.";
 RN Genome Res. 10:1617-1630(2000).

NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsushima S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RL sequencing pipeline with 384 multicapillary sequencer.";
 RN Genome Res. 10:1757-1771(2000).

NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh K., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

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EMBL; AK010826; BAB27208.1; -; mRNA.

EMBL; AK045095; BAC32219.1; -; mRNA.

HSSP; 088792; 1F97.

MGI; MGI:1933820; Jam2.

GO; GO:0005615; C:extracellular space; RCA.

GO; GO:0016021; C:integral to membrane; RCA.

InterPro; IPR007110; IG-like.

InterPro; IPR003599; IG-sub.

InterPro; IPR013106; IG V-set.

Pfam; PF07686; V-set; 1.

SMART; SM00409; IG; 1.

PROSITE; PS50835; IG_LIKE; 1.

Query Match 32.2%; Score 517.5; DB 2; Length 181;

Best Local Similarity 78.0%; Pred. NO. 1.7e-34;

Matches 103; Conservative 12; Mismatches 16; Indels 1; Gaps 1;

QY 1 MARRSRHRLLLLLRYLVVALGYHKAYGFSAPKD-QQVTVAYVOEAILCKTKPKTVSS 59

DB 1 MARSQGLMLLLHLLVLDYHKANGFSASAKHQRQEVTVIFQFEAILCKTKPKTTSS 60

QY 60 RLEWKKLGSRVSFVYVVOOTLQDGFKNRAEMIDFNIRIKNVTNRSDAGKYRCEVSAPSQG 119

DB 61 RLEWKKVGQSLVYVVOOTLQDGFKNRAEMIDFNIRIKNVTNRSDAGKYRCEVSAPSQG 120

QY 120 NLEEDTVTLEVL 131

DB 121 NLEQDKVLEVL 132

RESULT 6

ID JAM3 MOUSE STANDARD; PRT; 310 AA.

AC Q9DBE7; Q8BT59; Q9D1M9; Q9EPK4;

DT 10-MAY-2005, integrated into UniProtKB/Swiss-Prot.

DT 10-MAY-2005, sequence version 2.

DE 30-MAY-2006, entry version 35.

DE Junctional adhesion molecule C precursor (JAM-C) (Junctional adhesion

DE molecule 3) (JAM-3) (JAM-2).

GN Name=Jam3;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidae; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA].

RX MEDLINE=20489356; PubMed=11036763;

RA Aurrand-Lions M.A., Duncan L., Du Pasquier L., Imhof B.A.;

RT "Cloning of JAM-2 and JAM-3: an emerging junctional adhesion molecular

RT family?";

RL Curr. Top. Microbiol. Immunol. 251:91-98(2000).

RN [2]

RP NUCLEOTIDE SEQUENCE [MRNA].

RX MEDLINE=21264728; PubMed=11053409; DOI=10.1074/jbc.M005458200;

RA Aurrand-Lions M.A., Duncan L., Ballestrin C., Imhof B.A.;

RT "JAM-2, a novel immunoglobulin superfamily molecule, expressed by

RT endothelial and lymphatic cells.";

RL J. Biol. Chem. 276:2733-2741(2001).

RN [3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RC STRAIN=C57BL/6J; TISSUE=Embryo, Small intestine, and Wolffian duct;

RA Santoso S., Sachs U.J.H., Kroll H., Linder M., Ruf A., Preissner K.T.,
 RA Chavakis T.;
 RT "The junctional adhesion molecule 3 (JAM-3) on human platelets is a
 RT counterreceptor for the leukocyte integrin Mac-1";
 RL J. Exp. Med. 196:679-691(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE [MRNA], AND TISSUE SPECIFICITY.
 RX MEDLINE=21945252; PubMed=11944976; DOI=10.1006/geno.2002.6742;
 RA Phillips H.M., Renforth G.L., Spalluto C., Hearn T., Curtis A.R.J.,
 RA Craven L., Havarani B., Clement-Jones M., English C., Stumper O.,
 RA Salmon T., Hutchinson S., Jackson M.S., Wilson D.I.;
 RT "Narrowing the critical region within 11q24-qter for hypoplastic left
 RT heart and identification of a candidate gene, JAM3, expressed during
 RT cardiogenesis";
 RL Genomics 79:475-478(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hotuta T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Inose N.,
 RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Momiya H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takenoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs";
 RL Nat. Genet. 36:40-45(2004).
 RN [6]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
 RA Huang A., Kim H.S., Klinowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M.R., Robble E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Wandlen R.L., Watanabe C., Wiedand D., Woods K., Xie M.-H.,
 RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
 RA Wood W.I., Godowski P.J., Gray A.M.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment";
 RL Genome Res. 13:2265-2270(2003).
 RN [7]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Eye, and Uterus;
 RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buttsfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP PROTEIN SEQUENCE OF 32-46.
 RX PubMed=15340161; DOI=10.1110/ps.04682504;
 RA Zhang Z., Henzel W.J.;
 RT "Signal peptide prediction based on analysis of experimentally
 RT verified cleavage sites";
 RL Protein Sci. 13:2819-2824(2004).
 RN [9]
 RP REVIEW, AND NOMENCLATURE.
 RX MEDLINE=22695901; PubMed=12810109; DOI=10.1016/S1471-4906(03)00117-0;
 RA Muller W.A.;
 RT "Leukocyte-endothelial-cell interactions in leukocyte transmigration
 RT and the inflammatory response";
 RL Trends Immunol. 24:327-334(2003).
 CC -|- FUNCTION: May participate in cell-cell adhesion distinct from
 CC tight junctions.
 CC -|- SUBUNIT: Interacts with JAM2.
 CC -|- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
 CC protein (Potential).
 CC -|- TISSUE SPECIFICITY: Widely expressed. Highest expression in
 CC placenta, brain and kidney.
 CC -|- SIMILARITY: Belongs to the immunoglobulin superfamily.
 CC -|- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)
 CC domain.
 CC -|- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)
 CC domain.
 CC -----
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 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AF356518; AAK27221.1; -; mRNA.
 DR EMBL; AJ344431; CAC69845.1; -; mRNA.
 DR EMBL; AF448478; AAM20925.1; -; mRNA.
 DR EMBL; AJ416101; CAC94776.1; ALT INIT; mRNA.
 DR EMBL; AK074769; BAC11195.1; -; mRNA.
 DR EMBL; AK075309; BAC11538.1; -; mRNA.
 DR EMBL; AY358335; AAQ88701.1; -; mRNA.
 DR EMBL; BC010690; AAH10690.1; -; mRNA.
 DR EMBL; BC012147; AAH12147.1; -; mRNA.
 DR HSSP; O88792; IF97.
 DR Ensembl; ENSG00000166086; Homo sapiens.
 DR HGNC; HGNC:15532; JAM3.
 DR MIM; 606871; Gene.
 DR RZPD-ProtExp; W1215; -.
 DR RZPD-ProtExp; W2707; -.
 DR InterPro; IPR013151; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003599; Ig sub.
 DR InterPro; IPR003598; Ig sub2.
 DR InterPro; IPR013106; Ig_v-set.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF07686; V-set; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS50835; IG LIKE; 2.
 KW Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
 KW Membrane; Signal; Transmembrane.

FT SIGNAL 1 31
FT CHAIN 32 310
FT FT
FT FT
FT TOPO DOM 32 241
FT TRANS MEM 242 262
FT TOPO DOM 263 310
FT DOMAIN 35 127
FT DOMAIN 139 236
FT CARBOHYD 104 104
FT CARBOHYD 192 192
FT DISULFID 53 115
FT DISULFID 160 219
FT CONFLICT 136 136
SQ SEQUENCE 310 AA; 35020 MW; CE39ADF33EALDAB9 CRC64;

Query Match 28.8%; Score 461.5; DB 1; Length 310;
Best Local Similarity 37.1%; Pred. No. 1.4e-29;
Matches 104; Conservative 52; Mismatches 103; Indels 21; Gaps 7;

QY 1 MARRSRHRL-----LRLRLVVALGYHKAAGFSAPKQDVVTAVEYQEAAILAC 50
DB 1 MALRRPRLRLCARLPDFLLLLFGCLIG-----AVNLKSNRPVQV--EFESVELSC 53
QY 51 -KPKTKVSSRLWKKL-GRSVFVYQOTLQGFKNRAEMI-DFNIRIKNVTRSDAGKY 107
DB 54 IITDSQTSDPRIWKIQDEQTYVFFDNKIQDLAGRAEILKTSKIMWVTRDSALY 113
QY 108 RCEVSAPEEQONLEEDVTTLVLPAPVPSCEVPSSALSGTVVELRCQKGNPAPY 167
DB 114 RCEVVARNDR-KEIDEIVIELTVQKPTVPCRVKPAVPGMAYLHCQSEGHPRPHYS 172
QY 168 WFKGIRLLEPRLGSQTSNYSYNTTKTGLQFNVTSLKDTGEYSCEARNVGVRRCPG 227
DB 173 WIRNDVPLPTSRANPRNRSFHLNSETGLVFTAVHDDSGQYCIASNDAGSARCEE 232
QY 228 KRMQVDDNLNIGITAAVAVVVALVSVCGLVGCYAOQKGYF 267
DB 233 QEMEYVDNLNIGIIGVLLVLAVALITLIGICCAVARGYF 272

RESULT 9
Q66J15_XENTR PRELIMINARY; PRT; 291 AA.
AC Q66J15,
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 27-JUN-2006, entry version 21.
DE MGC79514 protein.
GN Name=MGC79514;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Silurana.
OX NCBI_TaxID=8364;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Cell membrane; lipid-anchor; GPI-anchor (By
CC similarity).
CC
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; BC080901; AAH80901.1; -; mRNA.
DR UniGene; Str.24914; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR013151; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR013098; Ig_L-set.
DR InterPro; IPR003599; Ig_sub.
DR InterPro; IPR003598; Ig_sub2.
DR Pfam; PF07679; I-set; 1.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00408; Ig; 2.
DR SMART; SM00409; IgC2; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Cell adhesion; Immunoglobulin domain; Repeat.
SQ SEQUENCE 291 AA; 31538 MW; D6A3115178E222A6 CRC64;

Query Match 27.7%; Score 445; DB 2; Length 291;
Best Local Similarity 35.0%; Pred. No. 3e-28;
Matches 103; Conservative 57; Mismatches 120; Indels 14; Gaps 6;

QY 1 MARRSRHRLLLRLVVALGYHKAAGFSAPKQDVVTAVEYQEAAILACKTKTVSS 59
DB 1 MATASSNRGAVVL--GLLCACLTAAAPAGVSTP--NPTITVKQATADLTKYTSDFTKS 56
QY 60 RLEWKKLGRSVS--FVYQOTLQGFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAFSEQ 117
DB 57 RVWKFVNNQLTFVYVYDGLTASVYVNRATSPVQIILNQITSKDAGEYSCVTSVDSN 116
QY 118 GQNL-EEDVTTLVLPAPVPSCEVPSSALSGTVVELRCQKGNPAPYTFWFKDGI RLL 176
DB 117 GQTLGEAKIQLLVIVAPSPMAHVNTVTRTGSVAVELRCVETQGYPPPTFTWYQKAMP 176
QY 177 ENPRLGSQTSNYSYNTTKTGLQFNVTSLKDTGEYSCEARNVGVRRCPKRMQVDDLN 236
DB 177 PNPQ-----NATYTDPTNGLKFRVAASDSDGYCKAANSEGEQVSAIVRNVQDVN 230
QY 237 ISGIIAAVVVVALVSVCGLVGCYAOQKGYFSEKTSFKSNSSSKATMTSENQV 290
DB 231 VGIIVAAVVVLLILALIGFLWYVSRGLDKGNKVIYSPSETRSDKNFQ 284

RESULT 10
Q2VPP6_XENLA PRELIMINARY; PRT; 291 AA.
AC Q2VPP6;
DT 10-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 27-JUN-2006, entry version 9.
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]

GenCore version 6.2
 Copyright (c) 1993 - 2007 Bioceleration Ltd.
 OM protein - nucleic search, using frame plus p2n model
 Run on: April 1, 2007, 21:42:07 ; Search time 293 Seconds
 (without alignments)
 1992.444 Million cell updates/sec

Title: US-10-785-221A-9
 Perfect score: 1605
 Sequence: 1 MARSRHRLLLLLRYLVA.....TPVIPALMKAAAGSGRGQBF 312
 Scoring table: BLOSUM62

	Xgapop 10.0 , Xgapext 0.5	Ygapop 10.0 , Ygapext 0.5	Fgapop 6.0 , Fgapext 7.0	Delpop 6.0 , Delext 7.0
Searched:	1403666 seqs, 935554401 residues			
Total number of hits satisfying chosen parameters:	2807332			
Minimum DB seq length:	0			
Maximum DB seq length:	200000000			
Post-processing:	Minimum Match 0%			
	Maximum Match 100%			
	Listing first 1500 summaries			

Command line parameters:
 -THR=1 -MODEL=framet_p2n.model -DEV=xlp
 -Q=/abs/ABSSWEB_spool/US10785221/runat_29032007_171149_7135/app_query.fasta_1
 -DB=Issued Patents NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
 -LIST=1500 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEADSIZE=0 -MINLEN=0 -MAXLEN=2000000000
 -USER=US10785221 @CGN 1 1 541 @runat_29032007_171149_7135 -NCPU=6 -ICPU=3
 -NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
 -WARN TIMEOUT=30 -MINDIST=10 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
 Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match Length	ID	Description
RESULT 1				
Percent Similarity:	100.0%			Conservative: 0
Best Local Similarity:	100.0%			Mismatches: 0
Query Match:	100.0%			Indels: 0
RESULT 2				
Percent Similarity:	100.0%			Conservative: 0
Best Local Similarity:	100.0%			Mismatches: 0
Query Match:	100.0%			Indels: 0
RESULT 3				
Percent Similarity:	100.0%			Conservative: 0
Best Local Similarity:	100.0%			Mismatches: 0
Query Match:	100.0%			Indels: 0
RESULT 4				
Percent Similarity:	100.0%			Conservative: 0
Best Local Similarity:	100.0%			Mismatches: 0
Query Match:	100.0%			Indels: 0
RESULT 5				
Percent Similarity:	100.0%			Conservative: 0
Best Local Similarity:	100.0%			Mismatches: 0
Query Match:	100.0%			Indels: 0
RESULT 6				
Percent Similarity:	100.0%			Conservative: 0
Best Local Similarity:	100.0%			Mismatches: 0
Query Match:	100.0%			Indels: 0
RESULT 7				
Percent Similarity:	100.0%			Conservative: 0
Best Local Similarity:	100.0%			Mismatches: 0
Query Match:	100.0%			Indels: 0
RESULT 8				
Percent Similarity:	100.0%			Conservative: 0
Best Local Similarity:	100.0%			Mismatches: 0
Query Match:	100.0%			Indels: 0
RESULT 9				
Percent Similarity:	100.0%			Conservative: 0
Best Local Similarity:	100.0%			Mismatches: 0
Query Match:	100.0%			Indels: 0
RESULT 10				
Percent Similarity:	100.0%			Conservative: 0
Best Local Similarity:	100.0%			Mismatches: 0
Query Match:	100.0%			Indels: 0

	Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%		Mismatches:	0
Query Match:	100.0%		Indels:	0
RESULT 11				
Percent Similarity:	100.0%		Conservative:	0
Best Local Similarity:	100.0%		Mismatches:	0
Query Match:	100.0%		Indels:	0
RESULT 12				
Percent Similarity:	100.0%		Conservative:	0
Best Local Similarity:	100.0%		Mismatches:	0
Query Match:	100.0%		Indels:	0
RESULT 13				
Percent Similarity:	100.0%		Conservative:	0
Best Local Similarity:	100.0%		Mismatches:	0
Query Match:	100.0%		Indels:	0
RESULT 14				
Percent Similarity:	100.0%		Conservative:	0
Best Local Similarity:	100.0%		Mismatches:	0
Query Match:	100.0%		Indels:	0
RESULT 15				
Percent Similarity:	100.0%		Conservative:	0
Best Local Similarity:	100.0%		Mismatches:	0
Query Match:	100.0%		Indels:	0

GenCore version 6.2
Copyright (c) 1993 - 2007 Bioacceleration Ltd.
OM protein - nucleic search, using frame plus p2n model
Run on: April 3, 2007, 00:09:50 ; Search time 1436 Seconds
(without alignments)
2669.737 Million cell updates/sec

Title: US-10-785-221A-9
Perfect score: 1605
Sequence: 1 MARRSRHRLLLLLRLVVA.....TPVIPALWKAAGSGRGQEF 312
Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
Searched: 18892170 seqs, 6143817638 residues 37784340
Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Command line parameters:
-THR=1 -MODEL=frame+ p2n.model -DEV=xlh
-Q=/abes/ABSSWEB_spool/US10785221/runat_29032007_171350_7795/app_query.fasta_1
-DB=Published Applications NA Main -QFMT=fastap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cgi -LIST=1500 -DOCALIGN=200 -THR SCORE=DCT
-THR MAX=100 -THR MIN=0 -ALIGN=0 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=0
-USER=US10785221@CGN_1_1675@runat_29032007_171350_7795 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -MINDIST=10 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
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GenCore version 6.2
Copyright (c) 1993 - 2007 Bioceleration Ltd.
OM protein - nucleic search, using frame plus p2n model
Run on: April 3, 2007, 00:26:50 ; Search time 892 Seconds
(without alignments)
2639.336 Million cell updates/sec

Title: US-10-785-221A-9
Perfect score: 1605
Sequence: 1 MARRSRHRLLLRLYLVA.....TPVIPALWKAAGSGRGQEF 312
Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
Searched: 14153951 seqs, 377289607 residues
Total number of hits satisfying chosen parameters: 28307902
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Command line parameters:
-THR=1 -MODEL=frame_p2n.model -DEV=xlh
-Q=/abs/ABSSWEB spool/US10785221/runat_29032007_171354_7855/app_query.fasta.1
-DB=Published Applications NA New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cgi -LIST=1500 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=0 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=0 -MINLEN=0
-USER=US10785221_@CGN_1_1116_@runat_29032007_171354_7855 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -MINDIST=10 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
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GenCore version 6.2
Copyright (c) 1993 - 2007 Bioceleration Ltd.
OM protein - nucleic search, using frame_plus_p2n model
Run on: April 2, 2007, 23:25:15 ; Search time 6453 Seconds
(without alignments)
2826.446 Million cell updates/sec

Title: US-10-785-221A-9
Perfect score: 1605
Sequence: 1 MARRSRHRLLLLLRYLVVA.....TPVIPALWKAAGSGRGQEF 312
Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
Searched: 86534536 seqs, 29229259966 residues
Total number of hits satisfying chosen parameters: 173069072
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Command line parameters:
-THR=1 -MODEL=frame+ p2n.model -DEV=xlh
-Q=/abs/ABSSWEB_spool/US10785221/runat_29032007_171342_7735/app_query.fasta_1
-DB=Pending_Patents_NA_Main -QFMT=fastap -SUFFIX=p2n.rnpm -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=1500 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR_MIN=0 -ALIGN=0 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=0 -MINLEN=0
-USER=US10785221_@CGN_1_1_7855 @runat_29032007_171342_7735 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -MINDIST=10 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

No.	Score	Match	Length	ID	Description
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GenCore version 6.2
Copyright (c) 1993 - 2007 Bioceleration Ltd.
OM protein - nucleic search, using frame_plus_p2n model
Run on: April 2, 2007, 23:49:02 ; Search time 3040 Seconds
(without alignments)
884.648 Million cell updates/sec

Title: US-10-785-221A-9
Perfect score: 1605
Sequence: 1 MARSRHRLLLLLRYLVVA.....TPVIPALWKAAGSGRQGF 312
Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
Searched: 10417259 seqs, 4309825506 residues 20834384
Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Command line parameters:
-THR=4 -MODEL=frame_plus_p2n.model -DEV=SOFT
-Q=/abss/ABSSWEB_spool/US10785221/runat_29032007_171345_7746/app_query.fasta_1
-DB=Pending Patents NA New -QFMT=fastap -SUFFIX=p2n.rnpn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=1500 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=0 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=0 -MINLEN=0
-USER=US10785221.CCGW_1_1072 @runat_29032007_171345_7746 -NCPU=6 -NO_MMAP
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

No.	Score	Match	Length	ID	Description
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GenCore version 6.2
 Copyright (c) 1993 - 2007 Bioceleration Ltd.
 OM protein - nucleic search, using frame_plus_p2n model
 Run on: April 2, 2007, 22:48:13 ; Search time 13890 Seconds
 (without alignments)
 1393.578 Million cell updates/sec

Title: US-10-785-221A-9
 Perfect score: 1605
 Sequence: 1 MARSRHRLLLLLLYLVA.....TFVIPALWKAAGSGRQGF 312
 Scoring table: BLOSUM62
 Xgapop 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 53585215 seqs, 31020513797 residues
 Total number of hits satisfying chosen parameters: 107169730
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1500 summaries

Command line parameters:
 -THR=4 -MODEL=frame+_p2n.model -DEV=SOFT
 -Q=/abs/ABSWEB_spool/US10785221/runat_29032007_171142_7077/app_query.fasta_1
 -DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1500
 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
 -HOST=ad2 -USER=US10785221 @CGN_1_1_7765 @runat_29032007_171142_7077 -NCPU=6
 -NO MAP -NEG SCORES=0 -WAIT -LONGLOG -MINDIST=10 -XGAPOF=10 -XGAPEXT=0.5
 -FGAPOF=6 -FGAPEXT=7 -YGAPOF=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1	Percent Similarity: 98.3%	Conservative: 1				
	Best Local Similarity: 97.9%	Mismatches: 1				
	Query Match: 89.3%	Indels: 4				
RESULT 2	Percent Similarity: 98.3%	Conservative: 1				
	Best Local Similarity: 97.9%	Mismatches: 1				
	Query Match: 89.3%	Indels: 4				
RESULT 3	Percent Similarity: 98.3%	Conservative: 1				
	Best Local Similarity: 97.9%	Mismatches: 1				
	Query Match: 89.3%	Indels: 4				
RESULT 4	Percent Similarity: 98.3%	Conservative: 1				
	Best Local Similarity: 97.9%	Mismatches: 1				
	Query Match: 89.3%	Indels: 4				
RESULT 5	Percent Similarity: 81.0%	Conservative: 2				
	Best Local Similarity: 80.4%	Mismatches: 3				
	Query Match: 86.9%	Indels: 64				
RESULT 6	Percent Similarity: 99.3%	Conservative: 1				
	Best Local Similarity: 98.9%	Mismatches: 2				
	Query Match: 86.2%	Indels: 0				
RESULT 7	Percent Similarity: 98.8%	Conservative: 0				
	Best Local Similarity: 98.8%	Mismatches: 3				
	Query Match: 82.1%	Indels: 0				
RESULT 8	Percent Similarity: 93.4%	Conservative: 16				
	Best Local Similarity: 87.8%	Mismatches: 19				
	Query Match: 81.8%	Indels: 0				
RESULT 9	Percent Similarity: 96.9%	Conservative: 0				
	Best Local Similarity: 96.9%	Mismatches: 7				
	Query Match: 79.7%	Indels: 1				
RESULT 10	Percent Similarity: 96.2%	Conservative: 15				

Best Local Similarity: 90.5%
 Query Match: 77.4%
 RESULT 11
 Percent Similarity: 96.9%
 Best Local Similarity: 92.5%
 Query Match: 76.3%
 RESULT 12
 Percent Similarity: 95.0%
 Best Local Similarity: 90.0%
 Query Match: 76.1%
 RESULT 13
 Percent Similarity: 97.5%
 Best Local Similarity: 97.5%
 Query Match: 74.0%
 RESULT 14
 Percent Similarity: 87.2%
 Best Local Similarity: 78.5%
 Query Match: 73.0%
 RESULT 15
 Percent Similarity: 87.2%
 Best Local Similarity: 78.5%
 Query Match: 73.0%

Mismatches: 10
 Indels: 0
 Conservative: 11
 Mismatches: 8
 Indels: 0
 Conservative: 13
 Mismatches: 13
 Indels: 0
 Conservative: 0
 Mismatches: 5
 Indels: 2
 Conservative: 25
 Mismatches: 35
 Indels: 2
 Conservative: 25
 Mismatches: 35
 Indels: 2

OM protein - protein search, using sw model
 Run on: April 10, 2007, 16:34:57 ; Search time 232 Seconds
 (without alignments)
 658.069 Million cell updates/sec

Title: US-10-785-221A-9
 Perfect score: 1605
 Sequence: 1 WARSRHRLLLLLLLRYLVA.....TPVIPALWKAAGSGRQGEF 312
 Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5
 Total number of hits satisfying chosen parameters: 2782304
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000
 Post-processing: Minimum Match 0%

Database :
 Listing first 1500 summaries
 A_Geneseq 200701:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*
 11: Geneseqp2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAY23324	standard; protein; 312 AA.				
DE	A33	related antigen PRO245.				
PN	WO9927098-A2.					
PD	03-JUN-1999.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1605;	DB 2;	Length 312;		
Best Local Similarity	100.0%;	Pred. No. 5.9e-123;				
RESULT 2						
ID	AAY08060	standard; protein; 312 AA.				
DE	Human PRO245	protein.				
PN	WO9914241-A2.					
PD	25-MAR-1999.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1605;	DB 2;	Length 312;		
Best Local Similarity	100.0%;	Pred. No. 5.9e-123;				
RESULT 3						
ID	AAY13354	standard; protein; 312 AA.				
DE	Amino acid sequence of protein PRO245.					
PN	WO9914328-A2.					
PD	25-MAR-1999.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1605;	DB 2;	Length 312;		
Best Local Similarity	100.0%;	Pred. No. 5.9e-123;				
RESULT 4						
ID	AAB33421	standard; protein; 312 AA.				
DE	Human PRO245	protein UNQ219 SEQ ID NO:36.				
PN	WO200053758-A2.					
PD	14-SEP-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1605;	DB 2;	Length 312;		
Best Local Similarity	100.0%;	Pred. No. 5.9e-123;				
RESULT 5						
ID	AAY70668	standard; protein; 312 AA.				
DE	Human PRO245	protein.				
PN	WO200015797-A2.					
PD	23-MAR-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1605;	DB 3;	Length 312;		
Best Local Similarity	100.0%;	Pred. No. 5.9e-123;				
RESULT 6						
ID	AAB24401	standard; protein; 312 AA.				

DE Human PRO245 protein sequence SEQ ID NO:67.
 PN WO200032221-A2.
 PD 08-JUN-2000.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 3; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 7
 ID ADC78384 standard; protein; 312 AA.
 DE Human PRO245 protein.
 PN WO200015796-A2.
 PD 23-MAR-2000.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 3; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 8
 ID AAB80222 standard; protein; 312 AA.
 DE Human PRO245 protein.
 PN WO200104311-A1.
 PD 18-JAN-2001.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 4; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 9
 ID AAU00821 standard; protein; 312 AA.
 DE Human immune response protein PRO245 (UNQ219).
 PN WO200119991-A1.
 PD 22-MAR-2001.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 4; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 10
 ID AAU12339 standard; protein; 312 AA.
 DE Human PRO245 polypeptide sequence.
 PN WO200140466-A2.
 PD 07-JUN-2001.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 4; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 11
 ID AAB53081 standard; protein; 312 AA.
 DE Human angiogenesis-associated protein PRO245, SEQ ID NO:91.
 PN WO200053753-A2.
 PD 14-SEP-2000.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 4; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 12
 ID ABU71600 standard; protein; 312 AA.
 DE Human PRO polypeptide #11.
 PN US2002146709-A1.
 PD 10-OCT-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 6; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 13
 ID ABO17783 standard; protein; 312 AA.
 DE Novel human secreted and transmembrane protein PRO245.
 PN US2003032156-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 6; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 14
 ID ABU71455 standard; protein; 312 AA.
 DE Human PRO polypeptide #11.
 PN US2002192659-A1.
 PD 19-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 6; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 15
 ID ABU81037 standard; protein; 312 AA.
 DE Human PRO polypeptide #168.

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PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1605; DB 6; Length 312;
RESULT 16
ID ABU71901 standard; protein; 312 AA.
DE Human secreted/transmembrane protein PRO245.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1605; DB 6; Length 312;
RESULT 17
ID AB001784 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1605; DB 6; Length 312;
RESULT 18
ID ABU66737 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1605; DB 6; Length 312;
RESULT 19
ID ABU54357 standard; protein; 312 AA.
DE Human secreted/transmembrane protein PRO245.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1605; DB 6; Length 312;
RESULT 20
ID AB047372 standard; protein; 312 AA.
DE Human secreted/transmembrane polypeptide PRO245.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1605; DB 6; Length 312;
RESULT 21
ID ABU59818 standard; protein; 312 AA.
DE Novel secreted and transmembrane protein PRO245.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1605; DB 6; Length 312;
RESULT 22
ID AB025008 standard; protein; 312 AA.
DE Human secreted/transmembrane protein (PRO) #168.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1605; DB 6; Length 312;
RESULT 23
ID ABU64509 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1605; DB 6; Length 312;
RESULT 24
ID ABU67355 standard; protein; 312 AA.
DE Human secreted protein PRO245.
PN US2003023054-A1.

PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1605; DB 6; Length 312;
RESULT 25
ID AB014875 standard; protein; 312 AA.
DE Human secreted / transmembrane polypeptide PRO245.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1605; DB 6; Length 312;
RESULT 26
ID ABU07738 standard; protein; 312 AA.
DE Human A-33 related antigen PRO245.
PN US2002182206-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1605; DB 6; Length 312;
RESULT 27
ID ABU67013 standard; protein; 312 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 336.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1605; DB 6; Length 312;
RESULT 28
ID ABU69632 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1605; DB 6; Length 312;
RESULT 29
ID AB014814 standard; protein; 312 AA.
DE Human secreted / transmembrane polypeptide PRO245.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1605; DB 6; Length 312;
RESULT 30
ID ADA45855 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1605; DB 6; Length 312;
RESULT 31
ID ADA76286 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1605; DB 6; Length 312;
RESULT 32
ID ADB29269 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1605; DB 6; Length 312;
RESULT 33
ID ADA18936 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003054517-A1.
PD 20-MAR-2003.

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PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 6; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 34
 ID ADA61559 standard; protein; 312 AA.
 DE Homo sapiens.
 PN US2003049816-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 6; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 35
 ID ADB19344 standard; protein; 312 AA.
 DE Novel human secreted and transmembrane protein PRO245.
 PN US2003068796-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 6; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 36
 ID ADB27885 standard; protein; 312 AA.
 DE Human PRO polypeptide #168.
 PN US2003082704-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 6; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 37
 ID ADA86364 standard; protein; 312 AA.
 DE Novel human secreted and transmembrane protein PRO245.
 PN US2003082711-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 6; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 38
 ID ADB15928 standard; protein; 312 AA.
 DE Human PRO polypeptide #168.
 PN US2003087350-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 6; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 39
 ID ADA47714 standard; protein; 312 AA.
 DE Human PRO polypeptide #168.
 PN US2003073215-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 6; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 40
 ID ADA18125 standard; protein; 312 AA.
 DE Human secreted/transmembrane protein, #13.
 PN US2003039971-A1.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 6; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 41
 ID ABO32766 standard; protein; 312 AA.
 DE Human secreted/transmembrane protein PRO245.
 PN US2003045693-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 6; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 42
 ID ADA67509 standard; protein; 312 AA.
 DE Human PRO polypeptide #168.
 PN US2003068795-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1605; DB 6; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 43
 ID ADB30516 standard; protein; 312 AA.
 DE Human PRO polypeptide #168.
 PN US2003068794-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 6; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 44
 ID ADA85812 standard; protein; 312 AA.
 DE Novel human secreted and transmembrane protein PRO245.
 PN US2003082693-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 6; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 45
 ID ADA97024 standard; protein; 312 AA.
 DE Human PRO polypeptide #168.
 PN US2003082705-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 6; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 46
 ID ADA79328 standard; protein; 312 AA.
 DE Human PRO polypeptide #168.
 PN US2003082763-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 6; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 47
 ID ADA87467 standard; protein; 312 AA.
 DE Novel human secreted and transmembrane protein PRO245.
 PN US2003087345-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 6; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 48
 ID ADB16669 standard; protein; 312 AA.
 DE Human PRO polypeptide #168.
 PN US2003087349-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 6; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 49
 ID ABO34826 standard; protein; 312 AA.
 DE Human PRO polypeptide #11.
 PN US2003044793-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 6; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 50
 ID ADA16100 standard; protein; 312 AA.
 DE Human secreted/transmembrane protein, #13.
 PN US2003049621-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 6; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 51
 ID ADA91761 standard; protein; 312 AA.
 DE Novel human secreted and transmembrane protein PRO245.
 PN US2003082694-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 6; Length 312;


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Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 52
ID ADB14824 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 53
ID ADB18785 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 54
ID ADA94000 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 55
ID ADB19896 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 56
ID ADB13208 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 57
ID ABO43316 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 58
ID ADA74462 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 59
ID ADA42245 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 60
ID ADB24695 standard; protein; 312 AA.
DE Human PRO polypeptide SEQ ID NO 336.
PN US200307713-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;

Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 61
ID ADA82219 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 62
ID ADA75182 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 63
ID ADA95260 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 64
ID ADA84708 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 65
ID ABO17504 standard; protein; 312 AA.
DE Human PRO polypeptide #11.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 66
ID ADB29964 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 67
ID ADA80492 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 68
ID ADA75734 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 69
ID ADA46959 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 70
ID ADA46959 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
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ID ADB25255 standard; protein; 312 AA.
DE Human PRO polypeptide SEQ ID NO 336.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 71
ID ADA93431 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 72
ID ADB26781 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 73
ID ADB31068 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 74
ID ADA60996 standard; protein; 312 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 75
ID ADB24143 standard; protein; 312 AA.
DE Human PRO polypeptide SEQ ID NO 336.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 76
ID ADA96472 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 77
ID ADA81044 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 78
ID ADA95920 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 79
ID ADB26229 standard; protein; 312 AA.

DE Human PRO polypeptide #168.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 80
ID ADB21714 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 81
ID ADA77493 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 82
ID ADB18233 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 83
ID ADA86916 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 84
ID ADA16524 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 85
ID ADA12953 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 86
ID ADA41821 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 87
ID ADA8019 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 88
ID ADA46407 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.

PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 98
ID ABO17565 standard; protein; 312 AA.
DE Human PRO polypeptide #11.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 99
ID ADA66957 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 100
ID ADB22818 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US200307711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 101
ID ADB23591 standard; protein; 312 AA.
DE Human PRO polypeptide SEQ ID NO 336.
PN US200307712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 102
ID ADA92313 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 103
ID ADB15376 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 104
ID ADB38628 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 105
ID ADB38076 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 106
ID ADB6548 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 99
ID ADA17168 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 90
ID ADA42671 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 91
ID ADB28437 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 92
ID ADB28989 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 93
ID ADA76941 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 94
ID ADA88571 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 95
ID ADA97576 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 96
ID ADB27333 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003022339-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 97
ID ADB22266 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087344-A1.
PD 08-MAY-2003.

Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 107
ID ADB89628 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 108
ID ADB90360 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 109
ID ADB77590 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 110
ID ADB39461 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 111
ID ADB74726 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 112
ID ADB47084 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 113
ID ADB86691 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 114
ID ADB77296 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 115
ID ADB34453 standard; protein; 312 AA.
DE Human PRO polypeptide SEQ ID NO 336.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;

RESULT 116
ID ADB35557 standard; protein; 312 AA.
DE Human PRO polypeptide SEQ ID NO 336.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 117
ID ADB33901 standard; protein; 312 AA.
DE Human PRO polypeptide SEQ ID NO 336.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 118
ID ADB35005 standard; protein; 312 AA.
DE Human PRO polypeptide SEQ ID NO 336.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 119
ID ADB36109 standard; protein; 312 AA.
DE Human PRO polypeptide SEQ ID NO 336.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 120
ID ADB46504 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 121
ID ADC28372 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 122
ID ADC39572 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 123
ID ADC40086 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 124
ID ADC18914 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 125
ID ADB34453 standard; protein; 312 AA.
DE Human PRO polypeptide SEQ ID NO 336.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;

ID ADC34210 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 126
ID ADC29265 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 127
ID ADC28796 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 128
ID ADC40681 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 129
ID ADC19338 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 130
ID ADC33786 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 131
ID ADC12856 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 132
ID ADC50377 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 133
ID ADC71924 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 134
ID ADC59903 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 135
ID ADC52910 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein Seq ID336.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 136
ID ADC57264 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein Seq ID336.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 137
ID ADC60455 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 138
ID ADC50930 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 139
ID ADC65457 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 140
ID ADC54555 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein Seq ID336.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 141
ID ADC53516 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein Seq ID336.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 142
ID ADC59039 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein Seq ID336.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 143
ID ADC55917 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein Seq ID336.

PN US2003087360-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 7; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 144
 ID ADC58487 standard; protein; 312 AA.
 DE Novel human secreted and transmembrane protein Seq ID336.
 PN US2003087346-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 7; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 145
 ID ADC12308 standard; protein; 312 AA.
 DE Human secreted/transmembrane protein, #13.
 PN US2003082541-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 7; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 146
 ID ADD03161 standard; protein; 312 AA.
 DE Novel human secreted and transmembrane protein PRO245.
 PN US2003092104-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 7; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 147
 ID ADC90153 standard; protein; 312 AA.
 DE Novel human secreted and transmembrane protein PRO245.
 PN US2003087348-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 7; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 148
 ID ADC69572 standard; protein; 312 AA.
 DE Human PRO polypeptide #168.
 PN US2003194770-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 7; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 149
 ID ADC48461 standard; protein; 312 AA.
 DE Human PRO polypeptide #168.
 PN US2003194773-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 7; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 150
 ID ADD09990 standard; protein; 312 AA.
 DE Human PRO polypeptide #168.
 PN US2003194776-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 7; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 151
 ID ADD04565 standard; protein; 312 AA.
 DE Novel human secreted and transmembrane protein PRO245.
 PN US2003087354-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 7; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 152
 ID ADC80521 standard; protein; 312 AA.
 DE Novel human secreted and transmembrane protein PRO245.
 PN US2003092103-A1.

PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 7; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 153
 ID ADD11028 standard; protein; 312 AA.
 DE Human PRO polypeptide #168.
 PN US2003194774-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 7; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 154
 ID ADC47909 standard; protein; 312 AA.
 DE Human PRO polypeptide #168.
 PN US2003194771-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 7; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 155
 ID ADD04863 standard; protein; 312 AA.
 DE Human secreted/transmembrane protein, #13.
 PN US2003104469-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 7; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 156
 ID ADC79969 standard; protein; 312 AA.
 DE Novel human secreted and transmembrane protein PRO245.
 PN US2003087358-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 7; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 157
 ID ADD09438 standard; protein; 312 AA.
 DE Human PRO polypeptide #168.
 PN US2003194775-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 7; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 158
 ID ADD03869 standard; protein; 312 AA.
 DE Human secreted/transmembrane protein, #13.
 PN US2003104381-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 7; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 159
 ID ADD03445 standard; protein; 312 AA.
 DE Human secreted/transmembrane protein, #13.
 PN US2003108983-A1.
 PD 12-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 7; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 160
 ID ADD41151 standard; protein; 312 AA.
 DE Novel human secreted and transmembrane protein PRO245.
 PN US2003203438-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 7; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 161
 ID ADD52290 standard; protein; 312 AA.
 DE Human PRO polypeptide #168.
 PN US2003194769-A1.
 PD 16-OCT-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 162
ID ADD53030 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 163
ID ADD53582 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 164
ID ADD51738 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 165
ID ADD02537 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 166
ID ADD01971 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 167
ID ADD34153 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 168
ID ADD92470 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 169
ID ADD91366 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 170
ID ADE03980 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.

PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 171
ID ADE32277 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 172
ID ADE22209 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 173
ID ADD79433 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 174
ID ADE41969 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 175
ID ADE17786 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 176
ID ADD91918 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 177
ID ADE33381 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 178
ID ADE33933 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 179
ID ADD79985 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
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Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 180
ID ADE93022 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 181
ID ADE19442 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 182
ID ADE34697 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 183
ID ADE18890 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 184
ID ADE43086 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 185
ID ADE95875 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 186
ID ADE22761 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 187
ID ADD78879 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 188
ID ADE32829 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;

RESULT 189
ID ADE42521 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 190
ID ADD80537 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 191
ID ADD89565 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 192
ID ADE40849 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 193
ID ADE04648 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 194
ID ADE92777 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 195
ID ADG21486 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 196
ID ADG23127 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 197
ID ADE97462 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 198
ID ADE97462 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 199

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ID ADG80526 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 199
ID ADG79974 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 200
ID ADH62536 standard; protein; 312 AA.
DE Human PRO245 protein encoded by DNA35638 cDNA.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUNA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 201
ID ADH59180 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 202
ID ADH55266 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 203
ID ADH55818 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 204
ID ADI37959 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 205
ID ADI64986 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 206
ID ADH81899 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 207
ID ADH81347 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 208
ID ADJ26227 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 209
ID ADM82516 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 210
ID ADNI5915 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 211
ID ADNI6544 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 212
ID ADNI5363 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 213
ID ADNI4811 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 214
ID ADI64037 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 215
ID ADI63485 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207387-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 216
ID ADC81073 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 217
ID ADE79142 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 218
ID ADD76521 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 219
ID ADD87885 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 220
ID ADD86289 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 221
ID ADE79566 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 222
ID ADE75737 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 223
ID ADE73242 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 224
ID ADE23313 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 225
ID ADE23865 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 226
ID ADE24508 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 227
ID ADD87333 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 228
ID ADE89199 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 229
ID ADE73777 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 230
ID ADE18338 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 231
ID ADE88647 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 232
ID ADE99331 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 233
ID ADE94667 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;

Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 234
ID ADE91078 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #168.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 235
ID ADE95219 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 236
ID ADE93329 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 237
ID ADF34910 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 238
ID ADE98450 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 239
ID ADE92225 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 240
ID ADE90526 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 241
ID ADE91673 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 242
ID ADE98877 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 243
ID ADG40347 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 244
ID ADF73741 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 245
ID ADG02252 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 246
ID ADG22038 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 247
ID ADG20108 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 248
ID ADF98014 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 249
ID ADG24231 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 250
ID ADF98585 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 251
ID ADG03416 standard; protein; 312 AA.
DE Human PRO polypeptide #168.

PN US2003207351-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 252
 ID ADF99137 standard; protein; 312 AA.
 DE Human PRO polypeptide #168.
 PN US2003207353-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 253
 ID ADG16722 standard; protein; 312 AA.
 DE Human PRO polypeptide #168.
 PN US2003207359-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 254
 ID ADG05181 standard; protein; 312 AA.
 DE Human PRO polypeptide #168.
 PN US2003207375-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 255
 ID ADG19448 standard; protein; 312 AA.
 DE Human PRO polypeptide #168.
 PN US2003207425-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 256
 ID ADF73317 standard; protein; 312 AA.
 DE Human secreted/transmembrane protein, #13.
 PN US2003166051-A1.
 PD 04-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 257
 ID ADG13285 standard; protein; 312 AA.
 DE Human PRO polypeptide #168.
 PN US2003207357-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 258
 ID ADG08342 standard; protein; 312 AA.
 DE Novel human secreted and transmembrane protein PRO245.
 PN US2003207424-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 259
 ID ADG15512 standard; protein; 312 AA.
 DE Human PRO polypeptide #168.
 PN US2003219885-A1.
 PD 27-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 260
 ID ADF96910 standard; protein; 312 AA.
 DE Human PRO polypeptide #168.
 PN US2003207371-A1.

PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 261
 ID ADG06095 standard; protein; 312 AA.
 DE Human PRO polypeptide #168.
 PN US2003207374-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 262
 ID ADG23679 standard; protein; 312 AA.
 DE Novel human secreted and transmembrane protein PRO245.
 PN US2003207389-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 263
 ID ADG03968 standard; protein; 312 AA.
 DE Human PRO polypeptide #168.
 PN US2003207423-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 264
 ID ADG24869 standard; protein; 312 AA.
 DE Novel human secreted and transmembrane protein PRO245.
 PN US2003207427-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 265
 ID ADG07166 standard; protein; 312 AA.
 DE Novel human secreted and transmembrane protein PRO245.
 PN US2003207350-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 266
 ID ADG07718 standard; protein; 312 AA.
 DE Novel human secreted and transmembrane protein PRO245.
 PN US2003207356-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 267
 ID ADG55213 standard; protein; 312 AA.
 DE Novel human secreted and transmembrane protein PRO245.
 PN US2003194778-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 268
 ID ADG60877 standard; protein; 312 AA.
 DE Novel human secreted and transmembrane protein PRO245.
 PN US2003207390-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 269
 ID ADG61981 standard; protein; 312 AA.
 DE Novel human secreted and transmembrane protein PRO245.
 PN US2003207428-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 270
ID ADG92160 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 271
ID ADG82182 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 272
ID ADG57421 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 273
ID ADG56869 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 274
ID ADG55765 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 275
ID ADG58525 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 276
ID ADG70891 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 277
ID ADG92587 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 278
ID ADG57973 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 279
ID ADG53557 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 280
ID ADG71443 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 281
ID ADG81630 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 282
ID ADH30592 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 283
ID ADH11959 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 284
ID ADG52381 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 285
ID ADG54109 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 286
ID ADG81078 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 287
ID ADG56317 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;

RESULT 288
ID ADH12583 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
ID ADG61429 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
ID ADH28516 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US20032022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
ID ADG54661 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
ID ADG59701 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
ID ADH20376 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
ID ADH07231 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
ID ADH59776 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
ID ADH06804 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.

PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 297
ID ADH1125 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 298
ID ADI18546 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 299
ID ADI65266 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 300
ID ADI37529 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 301
ID ADG09868 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 302
ID ADH97333 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 303
ID ADI15339 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 304
ID ADG09216 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 305
 ID ADI14671 standard; protein; 312 AA.
 DE Novel human secreted and transmembrane protein PRO245.
 PN US2003207383-A1.
 PD 06-NOV-2003.
 PA (GENE) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 306
 ID ADH60436 standard; protein; 312 AA.
 DE Human secreted/transmembrane protein, #13.
 PN US2004023331-A1.
 PD 05-FEB-2004.
 PA (DESN/) DESNOYERS L.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (MATH/) MATHER J P.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 307
 ID ADI18266 standard; protein; 312 AA.
 DE Novel human secreted and transmembrane protein PRO245.
 PN US2003207349-A1.
 PD 06-NOV-2003.
 PA (GENE) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 308
 ID ADJ99493 standard; protein; 312 AA.
 DE Human secreted/transmembrane protein, #13.
 PN US2003187238-A1.
 PD 02-OCT-2003.
 PA (GENE) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 309
 ID ADL08686 standard; protein; 312 AA.
 DE Human secreted/transmembrane protein, #13.
 PN US2003186358-A1.
 PD 02-OCT-2003.
 PA (GENE) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 310
 ID ADM25031 standard; protein; 312 AA.
 DE Human secreted/transmembrane protein, #13.
 PN US2003096233-A1.
 PD 22-MAY-2003.
 PA (GENE) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 311
 ID ADJ63547 standard; protein; 312 AA.
 DE Novel human secreted and transmembrane protein PRO245.
 PN US2004039164-A1.
 PD 26-FEB-2004.
 PA (GENE) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 312
 ID ADM29777 standard; protein; 312 AA.
 DE Human secreted/transmembrane protein, #13.
 PN US2003190611-A1.
 PD 09-OCT-2003.
 PA (GENE) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 313

ID ADJ77442 standard; protein; 312 AA.
 DE Human PRO polypeptide #168.
 PN US2004038336-A1.
 PD 26-FEB-2004.
 PA (GENE) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 314
 ID ADJ65564 standard; protein; 312 AA.
 DE Human PRO polypeptide #168.
 PN US2004038335-A1.
 PD 26-FEB-2004.
 PA (GENE) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 315
 ID ADM27700 standard; protein; 312 AA.
 DE Human PRO polypeptide #168.
 PN US2004048333-A1.
 PD 11-MAR-2004.
 PA (GENE) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 316
 ID ADM42424 standard; protein; 312 AA.
 DE Human PRO polypeptide #168.
 PN US2004058424-A1.
 PD 25-MAR-2004.
 PA (GENE) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 317
 ID ADO06099 standard; protein; 312 AA.
 DE Human PRO polypeptide #11.
 PN US6686451-B1.
 PD 03-FEB-2004.
 PA (GENE) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 318
 ID ADN35292 standard; protein; 312 AA.
 DE Human PRO245 protein.
 PN WO2004031105-A2.
 PD 15-APR-2004.
 PA (GENE) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 319
 ID ADM28286 standard; protein; 312 AA.
 DE Human PRO polypeptide #168.
 PN US2004077064-A1.
 PD 22-APR-2004.
 PA (GENE) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 320
 ID ADR10951 standard; protein; 312 AA.
 DE Human secreted/transmembrane protein, #13.
 PN US2004137561-A1.
 PD 15-JUL-2004.
 PA (GENE) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 321
 ID ADR17860 standard; protein; 312 AA.
 DE Human secreted/transmembrane protein, #13.
 PN US2004147017-A1.
 PD 29-JUL-2004.
 PA (ASHK/) ASHKENAZI A.
 PA (BOTS/) BOTSTEIN D.
 PA (DESN/) DESNOYERS L.
 PA (EATO/) EATON D L.
 PA (FERR/) FERRARA N.

PA (FILV/) FILVAROFF E.
 PA (FONG/) FONG S.
 PA (GAOW/) GAO W.
 PA (GERB/) GERBER H.
 PA (GERB/) GERRITSEN M E.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GRIM/) GRIMALDI C J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (KLJA/) KLJAVIN I J.
 PA (MATH/) MATHER J P.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (ROYM/) ROY M A.
 PA (STEW/) STEWART T A.
 PA (TUMA/) TUMAS D.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 322
 ID ADI95768 standard; protein; 312 AA.
 DE Human PRO polypeptide #168.
 PN US2003077659-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 323
 ID ADI96320 standard; protein; 312 AA.
 DE Novel human secreted and transmembrane protein PRO245.
 PN US2003207354-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 324
 ID ADI65693 standard; protein; 312 AA.
 DE Human secreted/transmembrane protein, #13.
 PN US2003148371-A1.
 PD 07-AUG-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 325
 ID ADI94237 standard; protein; 312 AA.
 DE Human PRO245 protein.
 PN AU2003259607-A1.
 PD 27-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 326
 ID ADS74499 standard; protein; 312 AA.
 DE Human secreted/transmembrane protein #13.
 PN US2004185531-A1.
 PD 23-SEP-2004.
 PA (ASHK/) ASHKENAZI A.
 PA (BOTS/) BOTSTEIN D.
 PA (DESN/) DESNOYERS L.
 PA (EATO/) EATON D L.
 PA (FERR/) FERRARA N.
 PA (FILV/) FILVAROFF E.
 PA (FONG/) FONG S.
 PA (GAOW/) GAO W.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GRIM/) GRIMALDI C J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.

PA (KLJA/) KLJAVIN I J.
 PA (MATH/) MATHER J P.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (ROYM/) ROY M A.
 PA (STEW/) STEWART T A.
 PA (TUMA/) TUMAS D.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 327
 ID ADS32272 standard; protein; 312 AA.
 DE Novel human secreted and transmembrane protein PRO245.
 PN US2004203125-A1.
 PD 14-OCT-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 328
 ID ADT03256 standard; protein; 312 AA.
 DE Human PRO polypeptide #168.
 PN US2004214269-A1.
 PD 28-OCT-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 329
 ID ADT03536 standard; protein; 312 AA.
 DE Human secreted/transmembrane protein, #13.
 PN US2003152922-A1.
 PD 14-AUG-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 330
 ID ADZ03307 standard; protein; 312 AA.
 DE Human secreted/transmembrane PRO245 protein.
 PN US2005074837-A1.
 PD 07-APR-2005.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 9; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 331
 ID AEA37774 standard; protein; 312 AA.
 DE Human secreted/transmembrane protein, #13.
 PN US2005112725-A1.
 PD 26-MAY-2005.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1605; DB 9; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.9e-123;
 RESULT 332
 ID AEB14053 standard; protein; 312 AA.
 DE Cancer cell diagnosis method-related human protein - SEQ ID 336.
 PN US2005153396-A1.
 PD 14-JUL-2005.
 PA (BAKE/) BAKER K P.
 PA (BERE/) BERESINI M.
 PA (DEFO/) DEFOGE L.
 PA (DESN/) DESNOYERS L.
 PA (FILV/) FILVAROFF E.
 PA (GAOW/) GAO W.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (SHER/) SHERWOOD S.
 PA (SMIT/) SMITH V.
 PA (STEW/) STEWART T A.
 PA (TUMA/) TUMAS D.
 PA (WATA/) WATANABE C K.
 PA (WOOD/) WOOD W I.
 PA (ZHAN/) ZHANG Z.

Query Match 100.0%; Score 1605; DB 9; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 333
ID AED23808 standard; protein; 312 AA.
DE Human secreted protein PRO 245, SEQ ID 64.
PN US2005214904-A1.
PD 29-SEP-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 9; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 334
ID AED86251 standard; protein; 312 AA.
DE Human PRO amino acid sequence, seq id 336.
PN US2005245730-A1.
PD 03-NOV-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 9; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 335
ID AEG68977 standard; protein; 312 AA.
DE Tyrosine kinase homologous PRO245 protein, SEQ ID 64.
PN US6974689-B1.
PD 13-DEC-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 10; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 336
ID AEG19650 standard; protein; 312 AA.
DE Human secreted protein PRO245.
PN WO2006026222-A2.
PD 09-MAR-2006.
PA (GETH) GENENTECH INC.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 100.0%; Score 1605; DB 10; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 337
ID AEG58198 standard; protein; 312 AA.
DE Human PRO245 polypeptide SEQ ID NO: 336.
PN US2006073568-A1.
PD 06-APR-2006.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 10; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 338
ID AEI43843 standard; protein; 312 AA.
DE Human cancer-related PRO protein amino acid sequence - SEQ ID 336.
PN US2006040351-A1.
PD 23-FEB-2006.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFOGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUNA/) TUNAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match 100.0%; Score 1605; DB 10; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 339
ID AEI23926 standard; protein; 312 AA.
DE Human secreted/transmembrane protein PRO245, SEQ ID NO:336.
PN EP1672070-A2.
PD 21-JUN-2006.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1605; DB 10; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 340
ID AEL49658 standard; protein; 312 AA.
DE Human PRO245/UNQ219 protein, SEQ ID NO: 9.
PN US2006233803-A1.
PD 19-OCT-2006.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 10; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
RESULT 341
ID AAB50904 standard; protein; 312 AA.
DE Human PRO245 protein.
PN WO200073452-A2.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 99.6%; Score 1599; DB 4; Length 312;
Best Local Similarity 99.7%; Pred. No. 1.8e-122;
RESULT 342
ID ADP56682 standard; protein; 323 AA.
DE Human junction adhesion molecule 2 splice variant (huJAM2sv) protein.
PN WO2004053058-A2.
PD 24-JUN-2004.
PA (LELIL) LILLY & CO ELI.
Query Match 99.0%; Score 1589; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 1.3e-121;
RESULT 343
ID AAW85457 standard; protein; 298 AA.
DE Secreted protein encoded by clone ct864_4.
PN WO9842739-A2.
PD 01-OCT-1998.
PA (GEMY) GENETICS INST INC.
Query Match 91.9%; Score 1475; DB 2; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.5e-112;
RESULT 344
ID AAU00512 standard; protein; 298 AA.
DE Human junctional adhesion protein (JAM2).
PN WO200114404-A1.
PD 01-MAR-2001.
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
Query Match 91.9%; Score 1475; DB 4; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.5e-112;
RESULT 345
ID ABP61801 standard; protein; 298 AA.
DE Human polypeptide SEQ ID NO 155.
PN US2002065394-A1.
PD 30-MAY-2002.
PA (JACO/) JACOBS K.
PA (MCCO/) MCCOY J M.
PA (LAVA/) LAVALLIE E R.
PA (COLL/) COLLINS-RACIE L A.
PA (EVAN/) EVANS C.
PA (NERE/) MERBERG D.
PA (TREA/) TREACY M.
PA (SPAU/) SPAULDING V.
Query Match 91.9%; Score 1475; DB 5; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.5e-112;
RESULT 346
ID ABR58532 standard; protein; 298 AA.
DE Human vascular endothelial junction-associated molecule protein.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 91.9%; Score 1475; DB 6; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.5e-112;
RESULT 347
ID ADI47178 standard; protein; 298 AA.
DE Human JAM-3 protein sequence.
PN WO2004003145-A2.
PD 08-JAN-2004.
PA (NAST-) NASTECH PHARM CO INC.
Query Match 91.9%; Score 1475; DB 8; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.5e-112;

Best Local Similarity 99.3%; Pred. No. 1.6e-111;
RESULT 354
ID ABR47926 standard; protein; 298 AA.
DE Human secreted protein, SEQ ID 817.
PD WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 91.3%; Score 1465; DB 6; Length 298;
Best Local Similarity 99.3%; Pred. No. 1.6e-111;
RESULT 355
ID ABR00172 standard; protein; 298 AA.
DE Human gene 162 encoded secreted protein HTEEB42, SEQ ID NO:461.
PD WO200276488-A1.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 91.3%; Score 1465; DB 6; Length 298;
Best Local Similarity 99.3%; Pred. No. 1.6e-111;
RESULT 356
ID ABU64994 standard; protein; 298 AA.
DE Human secreted protein gene 25, protein.
PD US2002172994-A1.
PD 21-NOV-2002.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
Query Match 91.3%; Score 1465; DB 6; Length 298;
Best Local Similarity 99.3%; Pred. No. 1.6e-111;
RESULT 357
ID ADB91670 standard; protein; 298 AA.
DE Human secreted protein #SEQ ID 616.
PD WO2003004622-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 91.3%; Score 1465; DB 7; Length 298;
Best Local Similarity 99.3%; Pred. No. 1.6e-111;
RESULT 358
ID ADC74331 standard; protein; 298 AA.
DE Human secreted protein - SEQ ID 964.
PD WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 91.3%; Score 1465; DB 7; Length 298;
Best Local Similarity 99.3%; Pred. No. 1.6e-111;
RESULT 359
ID ADG89803 standard; protein; 298 AA.
DE Human protein from secreted protein gene 25.
PD US2003225009-A1.
PD 04-DEC-2003.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.

PA (HAST/) HASTINGS G A.
Query Match 91.3%; Score 1465; DB 8; Length 298;
Best Local Similarity 99.3%; Pred. No. 1.6e-111;
RESULT 360
ID AED10240 standard; protein; 298 AA.
DE Human secreted polypeptide, SEQ ID 76.
PN US2005208621-A1.
PD 22-SEP-2005.
PA (HUWA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 91.3%; Score 1465; DB 9; Length 298;
RESULT 361
ID AEL94639 standard; protein; 298 AA.
DE Human secreted protein amino acid sequence - SEQ ID 820.
PN US2006246483-A1.
PD 02-NOV-2006.
Query Match
Best Local Similarity 91.3%; Score 1465; DB 10; Length 298;
RESULT 362
ID AAM23693 standard; protein; 303 AA.
DE Human EST encoded protein SEQ ID NO: 1218.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 90.9%; Score 1459.5; DB 4; Length 303;
RESULT 363
ID ABG22341 standard; protein; 388 AA.
DE Novel human diagnostic protein #22332.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 74.7%; Score 1199.5; DB 4; Length 388;
RESULT 364
ID AAO30179 standard; protein; 235 AA.
DE Human novel splice variant of VEJAM (NOJAM).
PN WO2003046180-A2.
PD 05-JUN-2003.
PA (GEST) GENSET SA.
Query Match
Best Local Similarity 74.6%; Score 1197; DB 6; Length 235;
RESULT 365
ID AAB27273 standard; protein; 298 AA.
DE Human confluency regulated adhesion molecule 2 #1.
PN WO200053749-A2.
PD 14-SEP-2000.
PA (RMFD-) RMF DICTAGENE SA.
Query Match
Best Local Similarity 71.3%; Score 1144; DB 3; Length 298;
RESULT 366
ID AAB27275 standard; protein; 298 AA.
DE Murine confluency regulated adhesion molecule 2.
PN WO200053749-A2.
PD 14-SEP-2000.
PA (RMFD-) RMF DICTAGENE SA.
Query Match
Best Local Similarity 71.3%; Score 1144; DB 3; Length 298;
RESULT 367
ID AAM41947 standard; protein; 222 AA.
DE Human polypeptide SEQ ID NO 6878.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 67.9%; Score 1090; DB 4; Length 222;
RESULT 368
ID AAB70500 standard; protein; 215 AA.
DE Angiogenesis protein AAA1 protein sequence (Fig 8).
PN WO200111086-A2.
PD 15-FEB-2001.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match
Best Local Similarity 65.8%; Score 1053; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 6.3e-78;
RESULT 369
ID AAB27277 standard; protein; 213 AA.
DE Human confluency regulated adhesion molecule 2 #2.
PN WO200053749-A2.
PD 14-SEP-2000.
PA (RMFD-) RMF DICTAGENE SA.
Query Match
Best Local Similarity 64.7%; Score 1039; DB 3; Length 213;
RESULT 370
ID ABG22338 standard; protein; 140 AA.
DE Novel human diagnostic protein #22329.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 40.5%; Score 649.5; DB 4; Length 140;
RESULT 371
ID AAM40161 standard; protein; 107 AA.
DE Human polypeptide SEQ ID NO 3306.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 30.8%; Score 494; DB 4; Length 107;
RESULT 372
ID AAB27278 standard; protein; 310 AA.
DE Murine confluency regulated adhesion molecule 1.
PN WO200053749-A2.
PD 14-SEP-2000.
PA (RMFD-) RMF DICTAGENE SA.
Query Match
Best Local Similarity 29.8%; Score 478; DB 3; Length 310;
RESULT 373
ID AAB27272 standard; protein; 310 AA.
DE Human confluency regulated adhesion molecule 1 #1.
PN WO200053749-A2.
PD 14-SEP-2000.
PA (RMFD-) RMF DICTAGENE SA.
Query Match
Best Local Similarity 29.8%; Score 478; DB 3; Length 310;
RESULT 374
ID ADP69027 standard; protein; 310 AA.
DE Human NOV2b protein SEQ ID NO:22.
PN WO2004055158-A2.
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 29.1%; Score 466.5; DB 8; Length 310;
RESULT 375
ID ADP69025 standard; protein; 310 AA.
DE Human NOV2a protein SEQ ID NO:20.
PN WO2004055158-A2.
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 29.0%; Score 465.5; DB 8; Length 310;
RESULT 376
ID ADP69035 standard; protein; 310 AA.
DE Human NOV2f protein SEQ ID NO:30.
PN WO2004055158-A2.
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 28.8%; Score 462.5; DB 8; Length 310;
RESULT 377
ID AAY96735 standard; protein; 310 AA.
DE PRO1868, an A33 antigen homologue.
PN WO200036102-A2.
PD 22-JUN-2000.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 28.8%; Score 461.5; DB 3; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;

RESULT 378
ID AAB33457 standard; protein; 310 AA.
DE Human PRO1868 protein UNQ859 SEQ ID NO:193.
PN WO200053758-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 3; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
ID AAB27276 standard; protein; 310 AA.
DE Human confluency regulated adhesion molecule 1 #2.
PN WO200053749-A2.
PD 14-SEP-2000.
PA (RMFD-) RMF DICTAGENE SA.
Query Match 28.8%; Score 461.5; DB 3; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
ID AAB80272 standard; protein; 310 AA.
DE Human PRO1868 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 4; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
ID AAM93905 standard; protein; 310 AA.
DE Human polypeptide, SEQ ID NO: 4051.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 28.8%; Score 461.5; DB 4; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
ID AAM93323 standard; protein; 310 AA.
DE Human polypeptide, SEQ ID NO: 2845.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 28.8%; Score 461.5; DB 4; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
ID AAB80383 standard; protein; 310 AA.
DE Secreted protein encoded by gene #13.
PN WO200107459-A1.
PD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 4; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
ID AAB80409 standard; protein; 310 AA.
DE Secreted protein encoded by gene #39.
PN WO200107459-A1.
PD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 4; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
ID AAB80408 standard; protein; 310 AA.
DE Secreted protein encoded by gene #38.
PN WO200107459-A1.
PD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 4; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
ID AAB95553 standard; protein; 310 AA.
DE Human angiogenesis related protein PRO1868 SEQ ID NO: 262.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 5; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
ID ABB95553 standard; protein; 310 AA.
DE Human angiogenesis related protein PRO1868 SEQ ID NO: 262.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.

ID ABG92709 standard; protein; 310 AA.
DE Human secreted protein PRO1868.
PN US2002098506-A1.
PD 25-JUL-2002.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 5; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
ID ABG91361 standard; protein; 310 AA.
DE Novel human secreted protein #7.
PN US2002098505-A1.
PD 25-JUL-2002.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 5; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
ID ABB84947 standard; protein; 310 AA.
DE Human PRO1868 protein sequence SEQ ID NO:262.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 5; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
ID ABG65297 standard; protein; 310 AA.
DE Human albumin fusion protein #1972.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 5; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
ID ABG65296 standard; protein; 310 AA.
DE Human albumin fusion protein #1971.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 5; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
ID ABG65298 standard; protein; 310 AA.
DE Human albumin fusion protein #1973.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 5; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
ID ABG31401 standard; protein; 310 AA.
DE Human PRO1868 polypeptide.
PN US2002098507-A1.
PD 25-JUL-2002.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 5; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
ID ABB95553 standard; protein; 310 AA.
DE Human angiogenesis related protein PRO1868 SEQ ID NO: 262.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.

PA (WATA/) WATANABE C K. 28.8%; Score 461.5; DB 5; Length 310;
 PA (WILL/) WILLIAMS P M. 28.8%; Score 461.5; DB 6; Length 310;
 PA (WOOD/) WOOD W I. 28.8%; Score 461.5; DB 5; Length 310;
 Query Match 37.1%; Pred. No. 3.1e-29;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 395
 ID ABU71650 standard; protein; 310 AA.
 DE Human PRO polypeptide #61.
 PN US2002146709-A1.
 PD 10-OCT-2002.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 396
 ID ABU72377 standard; protein; 310 AA.
 DE Novel human secreted and transmembrane protein PRO1868.
 PN US2002182618-A1.
 PD 05-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 397
 ID ABU80867 standard; protein; 310 AA.
 DE Human secreted and transmembrane polypeptide PRO1868.
 PN US2002192668-A1.
 PD 19-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 398
 ID ABO17884 standard; protein; 310 AA.
 DE Novel human secreted and transmembrane protein PRO1868.
 PN US2003032156-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 399
 ID ABU71505 standard; protein; 310 AA.
 DE Human PRO polypeptide #61.
 PN US2002192659-A1.
 PD 19-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 400
 ID ADA57610 standard; protein; 310 AA.
 DE Human secreted protein #592.
 PN WO2002102994-A2.
 PD 27-DEC-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 401
 ID ADA57611 standard; protein; 310 AA.
 DE Human secreted protein #592.
 PN WO2002102994-A2.
 PD 27-DEC-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 402
 ID ADA57309 standard; protein; 310 AA.
 DE Human secreted protein #592.
 PN WO2002102994-A2.
 PD 27-DEC-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 403
 ID ABP71277 standard; protein; 310 AA.
 DE Human junctional adhesion molecule 3 (JAM3).
 PN WO2003006673-A2.

PD 23-JAN-2003.
 PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 404
 ID ABU81138 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003004311-A1.
 PD 02-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 405
 ID ABU71951 standard; protein; 310 AA.
 DE Human secreted/transmembrane protein PRO1868.
 PN US2003003530-A1.
 PD 02-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 406
 ID ABO01834 standard; protein; 310 AA.
 DE Novel human secreted and transmembrane protein PRO1868.
 PN US2002197671-A1.
 PD 26-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 407
 ID ABU66838 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003036180-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 408
 ID ABU54407 standard; protein; 310 AA.
 DE Human secreted/transmembrane protein PRO1868.
 PN US2002132240-A1.
 PD 19-SEP-2002.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 409
 ID ABO47422 standard; protein; 310 AA.
 DE Human secreted/transmembrane polypeptide PRO1868.
 PN US2003044839-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 410
 ID ABG73314 standard; protein; 310 AA.
 DE Human PRO1868 polypeptide.
 PN US2002164646-A1.
 PD 07-NOV-2002.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 411
 ID ABUS9919 standard; protein; 310 AA.
 DE Novel secreted and transmembrane protein PRO1868.
 PN US2003017563-A1.
 PD 23-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 412
 ID ABO25109 standard; protein; 310 AA.
 DE Human secreted/transmembrane protein (PRO) #269.
 PN US2003036179-A1.
 PD 20-FEB-2003.

PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 413
 ID ABU64559 standard; protein; 310 AA.
 DE Human secreted/transmembrane protein, #63.
 PN US2002160374-A1.
 PD 31-OCT-2002.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 414
 ID ABU67405 standard; protein; 310 AA.
 DE Human secreted protein PRO1868.
 PN US2003023054-A1.
 PD 30-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 415
 ID ABO14925 standard; protein; 310 AA.
 DE Human secreted / transmembrane polypeptide PRO1868.
 PN US2003036060-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 416
 ID ABU60813 standard; protein; 310 AA.
 DE Human secreted/transmembrane protein, #7.
 PN US2002160392-A1.
 PD 31-OCT-2002.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 417
 ID ABU67114 standard; protein; 310 AA.
 DE Human secreted/transmembrane, PRO, protein SEQ ID 538.
 PN US2003032155-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 418
 ID ABU81236 standard; protein; 310 AA.
 DE Human PRO1917polypeptide.
 PN US2003032060-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 419
 ID ABU69682 standard; protein; 310 AA.
 DE Novel human secreted and transmembrane protein PRO1868+H30.
 PN US2003017463-A1.
 PD 23-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 420
 ID ABO14864 standard; protein; 310 AA.
 DE Human secreted / transmembrane polypeptide PRO1868.
 PN US2003027143-A1.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 421
 ID ADA46057 standard; protein; 310 AA.
 DE Novel human secreted and transmembrane protein PRO1868.
 PN US2003022328-A1.
 PD 30-JAN-2003.
 PA (GETH) GENENTECH INC.

Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 422
 ID ADA76488 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003073212-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 423
 ID ADB29627 standard; protein; 310 AA.
 DE Human secreted/transmembrane protein, #65.
 PN US2003092002-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 424
 ID ADA19138 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003054517-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 425
 ID ADA61761 standard; protein; 310 AA.
 DE Homo sapiens.
 PN US2003049816-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 426
 ID ADB19546 standard; protein; 310 AA.
 DE Novel human secreted and transmembrane protein PRO1868.
 PN US2003068796-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 427
 ID ADB28087 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003082704-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 428
 ID ADA86566 standard; protein; 310 AA.
 DE Novel human secreted and transmembrane protein PRO1868.
 PN US2003082711-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 429
 ID ADB16130 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003087350-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 430
 ID ADA47916 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003073215-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;

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Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 431
ID ADA18484 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003039371-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 432
ID ABO32816 standard; protein; 310 AA.
DE Human secreted/transmembrane protein PRO1868.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 433
ID ADA67711 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 434
ID ADB30718 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 435
ID ADA86014 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 436
ID ADA97226 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 437
ID ADA79530 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 438
ID ADA87669 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 439
ID ADB16871 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 440
ID ABO34876 standard; protein; 310 AA.
DE Human PRO polypeptide #61.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 441
ID ADA16459 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 442
ID ADA91963 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 443
ID ADB15026 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 444
ID ADB18987 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 445
ID ADA94202 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 446
ID ADB20098 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 447
ID ADB13410 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 448
ID ABO43417 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 449
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ID ADA74664 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 450
ID ADA42604 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 451
ID ADB24897 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077113-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 452
ID ADA82421 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 453
ID ADA75384 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 454
ID ADA85462 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 455
ID ADA84910 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 456
ID ABO17554 standard; protein; 310 AA.
DE Human PRO polypeptide #61.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 457
ID ADB30166 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 458
ID ADA80694 standard; protein; 310 AA.

DE Human PRO polypeptide #269.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 459
ID ADA75936 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 460
ID ADA47161 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 461
ID ADB25457 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 462
ID ADA93633 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 463
ID ADB26983 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 464
ID ADB31270 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 465
ID ABO62957 standard; protein; 310 AA.
DE Human PRO1868 protein.
PN US2003054447-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 466
ID ADA61198 standard; protein; 310 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 467
ID ADB24345 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.

PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 468
ID ADA96674 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 469
ID ADA81246 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 470
ID ADA96122 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 471
ID ADB26431 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 472
ID ADB21916 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 473
ID ADA77695 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 474
ID ADB18435 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 475
ID ADA87118 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 476
ID ADA16883 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003039969-A1.

PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 477
ID ADA13312 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 478
ID ADA42180 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 479
ID ADA98221 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 480
ID ADA46609 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 481
ID ADA17527 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 482
ID ADA43030 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 483
ID ADB28639 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 484
ID ADB29191 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 485
ID ABO01894 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003027256-A1.
PD 06-FEB-2003.

PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 7; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 486
 ID ADA77143 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003059909-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 7; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 487
 ID ADA88773 standard; protein; 310 AA.
 DE Novel human secreted and transmembrane protein PRO1868.
 PN US2003073213-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 7; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 488
 ID ADA97778 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003082686-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 7; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 489
 ID ADB27535 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003022239-A1.
 PD 30-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 7; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 490
 ID ADB22468 standard; protein; 310 AA.
 DE Novel human secreted and transmembrane protein PRO1868.
 PN US2003087344-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 7; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 491
 ID ABO17615 standard; protein; 310 AA.
 DE Human PRO polypeptide #61.
 PN US2003064923-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 7; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 492
 ID ADA67159 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003068793-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 7; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 493
 ID ADB23020 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003077711-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 7; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 494
 ID ADB23793 standard; protein; 310 AA.
 DE Human PRO polypeptide SEQ ID NO 538.
 PN US2003077712-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 7; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;

RESULT 495
 ID ADA92515 standard; protein; 310 AA.
 DE Novel human secreted and transmembrane protein PRO1868.
 PN US2003082712-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 7; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 496
 ID ADB15578 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003087352-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 7; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 497
 ID ADB38830 standard; protein; 310 AA.
 DE Novel human secreted and transmembrane protein PRO1868.
 PN US2003082766-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 7; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 498
 ID ADB38278 standard; protein; 310 AA.
 DE Novel human secreted and transmembrane protein PRO1868.
 PN US2003087347-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 7; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 499
 ID ADB66750 standard; protein; 310 AA.
 DE Novel human secreted and transmembrane protein PRO1868.
 PN US2003082689-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 7; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 500
 ID ADB98830 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003082698-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 7; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 501
 ID ADB90562 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003082762-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 7; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 502
 ID ADB77948 standard; protein; 310 AA.
 DE Human secreted/transmembrane protein, #65.
 PN US2003077654-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 7; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 503
 ID ADB39663 standard; protein; 310 AA.
 DE Novel human secreted and transmembrane protein PRO1868.
 PN US2003082764-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 7; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 504
 ID ADB39663 standard; protein; 310 AA.
 DE Novel human secreted and transmembrane protein PRO1868.
 PN US2003082764-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 7; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;

ID ADB75084 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 505
ID ADB47286 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 506
ID ADB86893 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 507
ID ADB77498 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 508
ID ADB34655 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US200307717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 509
ID ADB35759 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US200307719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 510
ID ADB34103 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US200307716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 511
ID ADB35207 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US200307718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 512
ID ADB36311 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US200307720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 513
ID ADB46706 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 514
ID ADC28731 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 515
ID ADC39931 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 516
ID ADC40445 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 517
ID ADC19269 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 518
ID ADC34569 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 519
ID ADC29624 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 520
ID ADC29155 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 521
ID ADC41040 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 522
ID ADC19697 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.

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PN US2003054441-A1.
PA (GETH ) GENENTECH INC.
  Query Match      28.8%; Score 461.5; DB 7; Length 310;
  Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 523
ID ADC34145 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      28.8%; Score 461.5; DB 7; Length 310;
  Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 524
ID ADC13215 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      28.8%; Score 461.5; DB 7; Length 310;
  Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 525
ID AAE3826 standard; protein; 310 AA.
DE Human PRO1868 protein.
PN US2003077657-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      28.8%; Score 461.5; DB 7; Length 310;
  Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 526
ID ADC05079 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      28.8%; Score 461.5; DB 7; Length 310;
  Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 527
ID ADC72126 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      28.8%; Score 461.5; DB 7; Length 310;
  Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 528
ID ADC60105 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      28.8%; Score 461.5; DB 7; Length 310;
  Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 529
ID ADC53112 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      28.8%; Score 461.5; DB 7; Length 310;
  Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 530
ID ADC57466 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      28.8%; Score 461.5; DB 7; Length 310;
  Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 531
ID ADC60657 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087367-A1.

PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      28.8%; Score 461.5; DB 7; Length 310;
  Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 532
ID ADC51132 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      28.8%; Score 461.5; DB 7; Length 310;
  Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 533
ID ADC65659 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      28.8%; Score 461.5; DB 7; Length 310;
  Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 534
ID ADC54757 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      28.8%; Score 461.5; DB 7; Length 310;
  Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 535
ID ADC53718 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      28.8%; Score 461.5; DB 7; Length 310;
  Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 536
ID ADC59241 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      28.8%; Score 461.5; DB 7; Length 310;
  Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 537
ID ADC56119 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      28.8%; Score 461.5; DB 7; Length 310;
  Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 538
ID ADC58689 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      28.8%; Score 461.5; DB 7; Length 310;
  Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 539
ID ADC12667 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      28.8%; Score 461.5; DB 7; Length 310;
  Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 540
ID ADC74383 standard; protein; 310 AA.
DE Human secreted protein - SEQ ID 1016.
PN WO2003038063-A2.
PD 08-MAY-2003.
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PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 541
ID ADC74606 standard; protein; 310 AA.
DE Human secreted protein - SEQ ID 1239.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 542
ID ADC74607 standard; protein; 310 AA.
DE Human secreted protein - SEQ ID 1240.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 543
ID ADD03363 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 544
ID ADC90355 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 545
ID ADC69774 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 546
ID ADC48663 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 547
ID ADD10192 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 548
ID ADD04767 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 549
ID ADC80723 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 550
ID ADD11230 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 551
ID ADD10551 standard; protein; 310 AA.
DE Human secreted/transmembrane PRO polypeptide #131.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 552
ID ADC48111 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 553
ID ADD05222 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 554
ID ADC80171 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 555
ID ADD11511 standard; protein; 310 AA.
DE Human secreted/transmembrane PRO polypeptide #131.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 556
ID ADD09640 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 557
ID ADD04228 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 558
ID ADD03804 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;

.Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 559
ID ADD41353 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 560
ID ADD52492 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 561
ID ADD53232 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 562
ID ADD53784 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 563
ID ADD37304 standard; protein; 310 AA.
DE Human secreted/transmembrane PRO polypeptide #131.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 564
ID ADD51940 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 565
ID ADD02739 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 566
ID ADD38106 standard; protein; 310 AA.
DE Human secreted protein #289.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 567
ID ADD38009 standard; protein; 310 AA.
DE Human secreted protein #192.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 568
ID ADD38105 standard; protein; 310 AA.
DE Human secreted protein #288.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 569
ID ADD02173 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 570
ID ADD54355 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 571
ID ADD92672 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 572
ID ADD91568 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 573
ID ADE04182 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 574
ID ADE32479 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 575
ID ADE22411 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 576
ID ADD79635 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 577

ID ADE42171 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 578
ID ADE17988 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 579
ID ADD92120 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 580
ID ADE33583 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 581
ID ADE34135 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 582
ID ADD80187 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 583
ID ADD93224 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 584
ID ADE19644 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 585
ID ADE35056 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 586
ID ADE19092 standard; protein; 310 AA.

DE Human PRO polypeptide #269.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 587
ID ADE43288 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 588
ID ADD96077 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 589
ID ADE22963 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 590
ID ADD79081 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 591
ID ADE33031 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 592
ID ADE42723 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 593
ID ADD80739 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 594
ID ADD89767 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 595
ID ADE41051 standard; protein; 310 AA.
DE Human PRO polypeptide #269.

PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 596
ID ADE04850 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 597
ID ADE92979 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 598
ID ADG21688 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 599
ID ADG23329 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 600
ID ADF97664 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 601
ID ADG80728 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 602
ID ADG80176 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 603
ID ADH62558 standard; protein; 310 AA.
DE Human PRO1868 protein.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.

Query Match	28.8%;	Score 461.5;	DB 7;	Length 310;
Best Local Similarity	37.1%;	Pred. No. 3.1e-29;		
RESULT 604				
ID ADH59539 standard; protein; 310 AA.				
DE Novel human secreted and transmembrane protein, #65.				
FN US2003039972-A1.				
PD 27-FEB-2003.				
PA (GETH) GENENTECH INC.				
Query Match	28.8%;	Score 461.5;	DB 7;	Length 310;
Best Local Similarity	37.1%;	Pred. No. 3.1e-29;		
RESULT 605				
ID ADH55468 standard; protein; 310 AA.				
DE Novel human secreted and transmembrane protein PRO1868.				
FN US20030207381-A1.				
PD 06-NOV-2003.				
PA (GETH) GENENTECH INC.				
Query Match	28.8%;	Score 461.5;	DB 7;	Length 310;
Best Local Similarity	37.1%;	Pred. No. 3.1e-29;		
RESULT 606				
ID ADH56020 standard; protein; 310 AA.				
DE Novel human secreted and transmembrane protein PRO1868.				
FN US2003207379-A1.				
PD 06-NOV-2003.				
PA (GETH) GENENTECH INC.				
Query Match	28.8%;	Score 461.5;	DB 7;	Length 310;
Best Local Similarity	37.1%;	Pred. No. 3.1e-29;		
RESULT 607				
ID ADI38318 standard; protein; 310 AA.				
DE Human secreted/transmembrane protein, #65.				
FN US2003054352-A1.				
PD 20-MAR-2003.				
PA (GETH) GENENTECH INC.				
Query Match	28.8%;	Score 461.5;	DB 7;	Length 310;
Best Local Similarity	37.1%;	Pred. No. 3.1e-29;		
RESULT 608				
ID ADI64239 standard; protein; 310 AA.				
DE Novel human secreted and transmembrane protein PRO1868.				
FN US2003207385-A1.				
PD 06-NOV-2003.				
PA (GETH) GENENTECH INC.				
Query Match	28.8%;	Score 461.5;	DB 7;	Length 310;
Best Local Similarity	37.1%;	Pred. No. 3.1e-29;		
RESULT 609				
ID ADI65188 standard; protein; 310 AA.				
DE Novel human secreted and transmembrane protein PRO1868.				
FN US2003207386-A1.				
PD 06-NOV-2003.				
PA (GETH) GENENTECH INC.				
Query Match	28.8%;	Score 461.5;	DB 7;	Length 310;
Best Local Similarity	37.1%;	Pred. No. 3.1e-29;		
RESULT 610				
ID ADI63687 standard; protein; 310 AA.				
DE Novel human secreted and transmembrane protein PRO1868.				
FN US2003207387-A1.				
PD 06-NOV-2003.				
PA (GETH) GENENTECH INC.				
Query Match	28.8%;	Score 461.5;	DB 7;	Length 310;
Best Local Similarity	37.1%;	Pred. No. 3.1e-29;		
RESULT 611				
ID ADH82101 standard; protein; 310 AA.				
DE Novel human secreted and transmembrane protein PRO1868.				
FN US2003207388-A1.				
PD 06-NOV-2003.				
PA (GETH) GENENTECH INC.				
Query Match	28.8%;	Score 461.5;	DB 7;	Length 310;
Best Local Similarity	37.1%;	Pred. No. 3.1e-29;		
RESULT 612				
ID ADH81549 standard; protein; 310 AA.				
DE Novel human secreted and transmembrane protein PRO1868.				
FN US2003207377-A1.				
PD 06-NOV-2003.				
PA (GETH) GENENTECH INC.				
Query Match	28.8%;	Score 461.5;	DB 7;	Length 310;
Best Local Similarity	37.1%;	Pred. No. 3.1e-29;		
RESULT 613				
ID ADH82101 standard; protein; 310 AA.				
DE Novel human secreted and transmembrane protein PRO1868.				
FN US2003207388-A1.				
PD 06-NOV-2003.				
PA (GETH) GENENTECH INC.				
Query Match	28.8%;	Score 461.5;	DB 7;	Length 310;
Best Local Similarity	37.1%;	Pred. No. 3.1e-29;		
RESULT 614				
ID ADH82101 standard; protein; 310 AA.				
DE Novel human secreted and transmembrane protein PRO1868.				
FN US2003207388-A1.				
PD 06-NOV-2003.				
PA (GETH) GENENTECH INC.				
Query Match	28.8%;	Score 461.5;	DB 7;	Length 310;
Best Local Similarity	37.1%;	Pred. No. 3.1e-29;		
RESULT 615				
ID ADH82101 standard; protein; 310 AA.				
DE Novel human secreted and transmembrane protein PRO1868.				
FN US2003207388-A1.				
PD 06-NOV-2003.				
PA (GETH) GENENTECH INC.				
Query Match	28.8%;	Score 461.5;	DB 7;	Length 310;
Best Local				

Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 613
ID ADJ58518 standard; protein; 310 AA.
DE Human PRO1868 protein.
PN US2003170864-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 614
ID ADJ26586 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003053439-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 615
ID ADM82718 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 616
ID ADN16117 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 617
ID ADN16746 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 618
ID ADN15565 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 619
ID ADN15013 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 620
ID ADC81275 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 621
ID ADE79501 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 622
ID ADD76723 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 623
ID ADD88087 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 624
ID ADD86491 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 625
ID ADE79925 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 626
ID ADE75939 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 627
ID ADE73601 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 628
ID ADE41512 standard; protein; 310 AA.
DE Human secreted/transmembrane PRO polypeptide #131.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 629
ID ADE3515 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 630
ID ADE24067 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 631

ID ADE24710 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 632
ID ADE87535 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 633
ID ADE89401 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 634
ID ADE74136 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 635
ID ADE18540 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 636
ID ADE88849 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 637
ID ADE99690 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 638
ID ADE94869 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 639
ID ADE91280 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 640
ID ADE95421 standard; protein; 310 AA.

DE Human PRO polypeptide #269.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 641
ID ADE93531 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 642
ID ADF35112 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 643
ID ADE98809 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 644
ID ADE92427 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 645
ID ADE90728 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 646
ID ADE91875 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 647
ID ADE99236 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 648
ID ADG40706 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.

PA (WOOD/) WOOD W I.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 649
ID ADF74100 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 650
ID ADG02454 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 651
ID ADG22240 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 652
ID ADG20310 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 653
ID ADF98216 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 654
ID ADG24433 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 655
ID ADF98787 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 656
ID ADG03618 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 657
ID ADF99339 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 658
ID ADG16924 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 659
ID ADG05383 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 660
ID ADG19650 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 661
ID ADF73676 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 662
ID ADG13487 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 663
ID ADG08544 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 664
ID ADG15714 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 665
ID ADF97112 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 666
ID ADG06297 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 667
ID ADF99339 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 667
ID ADG2384 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 668
ID ADG04170 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 669
ID ADG25071 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 670
ID ADG07368 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 671
ID ADG07920 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 672
ID ADG55415 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 673
ID ADG61079 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 674
ID ADG62183 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 675
ID ADG92519 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 676
ID ADG82384 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 677
ID ADG57623 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 678
ID ADG57071 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 679
ID ADG55967 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 680
ID ADG58727 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 681
ID ADG71093 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 682
ID ADG92946 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 683
ID ADG58175 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 684
ID ADG53759 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 685

ID ADG71645 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 696
ID ADG81832 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 697
ID ADH30794 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 698
ID ADH12161 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 699
ID ADG52583 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 699
ID ADG54311 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 691
ID ADG81280 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 692
ID ADG56519 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 693
ID ADH12785 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 694
ID ADG61631 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 695
ID ADH28718 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 696
ID ADG54863 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 697
ID ADG59903 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 698
ID ADH20735 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 699
ID ADH43695 standard; protein; 310 AA.
DE Human PRO polypeptide #131.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 700
ID ADH07590 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 701
ID ADH60135 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 702
ID ADH07163 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.

PA (GODD//) GODDARD A. 28.8%; Score 461.5; DB 8; Length 310;
 PA (GODO//) GODOWSKI P J.
 PA (GURN//) GURNEY A L.
 PA (MATH//) MATHER J P.
 PA (WILL//) WILLIAMS P M.
 PA (WOOD//) WOOD W I.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 703
 ID ADI18327 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003207361-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 704
 ID ADI18905 standard; protein; 310 AA.
 DE Human secreted/transmembrane protein, #65.
 PN US2003152999-A1.
 PD 14-AUG-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 705
 ID ADI65625 standard; protein; 310 AA.
 DE Human secreted/transmembrane protein, #65.
 PN US2003148419-A1.
 PD 07-AUG-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 706
 ID ADI37884 standard; protein; 310 AA.
 DE Human secreted/transmembrane protein, #65.
 PN US2003096340-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 707
 ID ADG10070 standard; protein; 310 AA.
 DE Novel human secreted and transmembrane protein PRO1868.
 PN US2004009548-A1.
 PD 15-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 708
 ID ADH97684 standard; protein; 310 AA.
 DE Human secreted/transmembrane protein, #65.
 PN US2003190610-A1.
 PD 09-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 709
 ID ADI15541 standard; protein; 310 AA.
 DE Novel human secreted and transmembrane protein PRO1868.
 PN US2003207382-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 710
 ID ADG09418 standard; protein; 310 AA.
 DE Novel human secreted and transmembrane protein PRO1868.
 PN US2004009547-A1.
 PD 15-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 711

ID ADI6052 standard; protein; 310 AA.
 DE Human secreted/transmembrane protein, #65.
 PN US2003148371-A1.
 PD 07-AUG-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 712
 ID ADI10341 standard; protein; 310 AA.
 DE Human PRO1868 protein from DNA7624-2515 clone.
 PN US2003228664-A1.
 PD 11-DEC-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 713
 ID ADI14873 standard; protein; 310 AA.
 DE Novel human secreted and transmembrane protein PRO1868.
 PN US2003207383-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 714
 ID ADH60795 standard; protein; 310 AA.
 DE Human secreted/transmembrane protein, #65.
 PN US2004023331-A1.
 PD 05-FEB-2004.
 PA (DESN//) DESNOYERS L.
 PA (GODD//) GODDARD A.
 PA (GODO//) GODOWSKI P J.
 PA (GURN//) GURNEY A L.
 PA (MATH//) MATHER J P.
 PA (WILL//) WILLIAMS P M.
 PA (WOOD//) WOOD W I.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 715
 ID ADI18468 standard; protein; 310 AA.
 DE Novel human secreted and transmembrane protein PRO1868.
 PN US2003207349-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 716
 ID ADJ9852 standard; protein; 310 AA.
 DE Human secreted/transmembrane protein, #65.
 PN US2003187238-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 717
 ID ADL09045 standard; protein; 310 AA.
 DE Human secreted/transmembrane protein, #65.
 PN US2003186358-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 718
 ID ADI47177 standard; protein; 310 AA.
 DE Human JAM-2 protein sequence.
 PN WO2004003145-A2.
 PD 08-JAN-2004.
 PA (NAST-) NASTECH PHARM CO INC.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 3.1e-29;
 RESULT 719
 ID ADM25386 standard; protein; 310 AA.
 DE Human secreted/transmembrane protein, #65.
 PN US2003096233-A1.

PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 720
ID ADJ63749 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 721
ID ADJ30136 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 722
ID ADJ78563 standard; protein; 310 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 2045.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 723
ID ADJ78564 standard; protein; 310 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 2046.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 724
ID ADJ78565 standard; protein; 310 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 2047.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 725
ID ADJ77644 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 726
ID ADX83040 standard; protein; 310 AA.
DE Human PRO polypeptide #131.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 727
ID ADJ65766 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 728
ID ADL30812 standard; protein; 310 AA.

DE Human protein encoded by a full length cDNA clone SeqID 2845.
PN EPI396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 729
ID ADL32018 standard; protein; 310 AA.
DE Human protein encoded by a full length cDNA clone SeqID 4051.
PN EPI396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 730
ID ADM27902 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 731
ID ADM2626 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 732
ID ADO06458 standard; protein; 310 AA.
DE Human PRO polypeptide #60.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 733
ID ADN35310 standard; protein; 310 AA.
DE Human PRO1868 protein.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 734
ID ADM28488 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 735
ID ADP69033 standard; protein; 310 AA.
DE Human NOV2e protein SEQ ID NO:28.
PN WO2004055158-A2.
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 736
ID ADRL1310 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 737
ID ADRI8219 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.

PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 738
ID ADI95970 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 739
ID ADI96522 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 740
ID ADS74858 standard; protein; 310 AA.
DE Human secreted/transmembrane protein #65.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 741
ID ADS32474 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2004203125-A1.
PD 14-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 742
ID AUT03458 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2004214269-A1.
PD 28-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 743
ID ADT03895 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 744
ID ADZ03509 standard; protein; 310 AA.
DE Human secreted/transmembrane PRO1868 protein.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 9; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 745
ID AEA38133 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2005112725-A1.
PD 28-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 9; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 746
ID AEB14255 standard; protein; 310 AA.
DE Cancer cell diagnosis method-related human protein - SEQ ID 538.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFORGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match 28.8%; Score 461.5; DB 9; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 747
ID AED24167 standard; protein; 310 AA.
DE Human secreted protein PRO 1868, SEQ ID 423.
PN US2005214904-A1.
PD 29-SEP-2005.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 9; Length 310;

Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 748
ID AED86453 standard; protein; 310 AA.
DE Human PRO amino acid sequence, seq id 538.
PN US2005245730-A1.
PD 03-NOV-2005.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 9; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 749
ID AEE69336 standard; protein; 310 AA.
DE Dayhoff homologous PRO1868 protein, SEQ ID 423.
PN US6974689-B1.
PD 13-DEC-2005.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 10; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 750
ID AEG58400 standard; protein; 310 AA.
DE Human PRO1868 polypeptide SEQ ID NO: 538.
PN US2006073568-A1.
PD 06-APR-2006.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 10; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 751
ID AEH08838 standard; protein; 310 AA.
DE Therapeutic protein HAPSA79, SEQ ID 2047.
PN US2006084794-A1.
PD 20-APR-2006.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 10; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 752
ID AEH08837 standard; protein; 310 AA.
DE Therapeutic protein HAPSA79, SEQ ID 2046.
PN US2006084794-A1.
PD 20-APR-2006.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 10; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 753
ID AEH08836 standard; protein; 310 AA.
DE Therapeutic protein HAPSA79, SEQ ID 2045.
PN US2006084794-A1.
PD 20-APR-2006.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 10; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 754
ID AEI44045 standard; protein; 310 AA.
DE Human cancer-related PRO protein amino acid sequence - SEQ ID 539.
PN US2006040351-A1.
PD 23-FEB-2006.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFOGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUNA/) TUNAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match 28.8%; Score 461.5; DB 10; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;

RESULT 755
ID AEI24128 standard; protein; 310 AA.
DE Human secreted/transmembrane protein PRO1868, SEQ ID NO:538.
PN EP1672070-A2.
PD 21-JUN-2006.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 10; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 756
ID AEL02318 standard; protein; 310 AA.
DE Human secreted protein amino acid sequence - SEQ ID 496.
PN US2006223090-A1.
PD 05-OCT-2006.
Query Match 28.8%; Score 461.5; DB 10; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 757
ID AEL02418 standard; protein; 310 AA.
DE Human secreted protein amino acid sequence - SEQ ID 596.
PN US2006223090-A1.
PD 05-OCT-2006.
Query Match 28.8%; Score 461.5; DB 10; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 758
ID AEL02417 standard; protein; 310 AA.
DE Human secreted protein amino acid sequence - SEQ ID 595.
PN US2006223090-A1.
PD 05-OCT-2006.
Query Match 28.8%; Score 461.5; DB 10; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 759
ID AEL29824 standard; protein; 310 AA.
DE Human secreted protein, SEQ ID 1804.
PN US2006223088-A1.
PD 05-OCT-2006.
Query Match 28.8%; Score 461.5; DB 10; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 760
ID AEL29519 standard; protein; 310 AA.
DE Human secreted protein, SEQ ID 1499.
PN US2006223088-A1.
PD 05-OCT-2006.
Query Match 28.8%; Score 461.5; DB 10; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 761
ID AEL29823 standard; protein; 310 AA.
DE Human secreted protein, SEQ ID 1803.
PN US2006223088-A1.
PD 05-OCT-2006.
Query Match 28.8%; Score 461.5; DB 10; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 762
ID AEL49680 standard; protein; 310 AA.
DE Human PRO1868 protein, SEQ ID NO: 31.
PN US2006233803-A1.
PD 19-OCT-2006.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 10; Length 310;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 763
ID AAB38383 standard; protein; 311 AA.
DE Human secreted protein encoded by gene 13 clone HAPSA79.
PN WO20061623-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 3; Length 311;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 764
ID AAB38384 standard; protein; 311 AA.
DE Human secreted protein encoded by gene 13 clone HAPSA79.
PN WO20061623-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 3; Length 311;

Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 765
ID AAB38333 standard; protein; 311 AA.
DE Human secreted protein encoded by gene 13 clone HAPSA79.
PN WO200061623-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 3; Length 311;
Best Local Similarity 37.1%; Pred. No. 3.1e-29;
RESULT 766
ID AAB80431 standard; peptide; 339 AA.
DE Gene #13 associated peptide #1.
PN WO200107459-A1.
PD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 4; Length 339;
Best Local Similarity 37.1%; Pred. No. 3.4e-29;
RESULT 767
ID AEG24802 standard; protein; 355 AA.
DE Human JAM3.
PN WO2006022636-A1.
PD 02-MAR-2006.
PA (SEQU-) SEQUENOM INC.
Query Match 28.8%; Score 461.5; DB 10; Length 355;
Best Local Similarity 37.1%; Pred. No. 3.6e-29;
RESULT 768
ID AED74320 standard; protein; 362 AA.
DE Human placental protein SEQ ID NO:1148.
PN US2005255114-A1.
PD 17-NOV-2005.
PA (NUVE-) NUVELO INC.
Query Match 28.8%; Score 461.5; DB 9; Length 362;
Best Local Similarity 37.1%; Pred. No. 3.7e-29;
RESULT 769
ID ABP41902 standard; protein; 329 AA.
DE Human ovarian antigen HISAFA60, SEQ ID NO:3034.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.7%; Score 460.5; DB 5; Length 329;
Best Local Similarity 37.9%; Pred. No. 4e-29;
RESULT 770
ID AAO16453 standard; protein; 310 AA.
DE Human junctional adhesion molecule 3 (huJAM3).
PN WO2003008541-A2.
PD 30-JAN-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 28.6%; Score 459.5; DB 6; Length 310;
Best Local Similarity 37.0%; Pred. No. 4.5e-29;
RESULT 771
ID AAY96294 standard; protein; 310 AA.
DE Human IGFAM-6 immunoglobulin.
PN WO200029583-A2.
PD 25-MAY-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 28.4%; Score 456.5; DB 3; Length 310;
Best Local Similarity 37.1%; Pred. No. 7.9e-29;
RESULT 772
ID ADP56683 standard; protein; 310 AA.
DE Human junction adhesion molecule 3 (huJAM3) full-length protein.
PN WO2004053058-A2.
PD 24-JUN-2004.
PA (ELIL) LILLY & CO ELI.
Query Match 28.4%; Score 456.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 7.9e-29;
RESULT 773
ID AAB39254 standard; protein; 285 AA.
DE Human secreted protein sequence encoded by gene 15 SEQ ID NO:134.
PN WO200056754-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.3%; Score 455; DB 3; Length 285;
Best Local Similarity 39.7%; Pred. No. 9.4e-29;
RESULT 774
ID AAO30255 standard; protein; 87 AA.
DE Human novel splice variant of VEJAM (NOJAM) fragment.
PN WO2003046180-A2.
PD 05-JUN-2003.
PA (GEST) GENSET SA.
Query Match 27.9%; Score 448; DB 6; Length 87;
Best Local Similarity 98.8%; Pred. No. 7.6e-29;
RESULT 775
ID ABB06037 standard; protein; 321 AA.
DE Human NS protein sequence SEQ ID NO:129.
PN WO200206315-A2.
PD 24-JAN-2002.
PA (COMP-) COMPUGEN LTD.
Query Match 27.7%; Score 444; DB 5; Length 321;
Best Local Similarity 35.8%; Pred. No. 8.7e-28;
RESULT 776
ID ADP29461 standard; protein; 90 AA.
DE Human secreted protein SEQ ID #1459.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 27.4%; Score 439; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 4.4e-28;
RESULT 777
ID AAU17996 standard; protein; 301 AA.
DE Human immunoglobulin polypeptide SEQ ID NO 141.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 25.5%; Score 409; DB 4; Length 301;
Best Local Similarity 34.3%; Pred. No. 5.9e-25;
RESULT 778
ID ABB10232 standard; protein; 301 AA.
DE Human CDNA SEQ ID NO: 540.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 25.5%; Score 409; DB 4; Length 301;
Best Local Similarity 34.3%; Pred. No. 5.9e-25;
RESULT 779
ID ABP66819 standard; protein; 301 AA.
DE Human polypeptide SEQ ID NO 540.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 25.5%; Score 409; DB 5; Length 301;
Best Local Similarity 34.3%; Pred. No. 5.9e-25;
RESULT 780
ID ADB31620 standard; protein; 301 AA.
DE Human novel protein SEQ ID NO 141.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 25.5%; Score 409; DB 7; Length 301;
Best Local Similarity 34.3%; Pred. No. 5.9e-25;
RESULT 781
ID ADR41522 standard; protein; 318 AA.
DE Human CD-like molecule HKACI03, SEQ ID NO:321.
PN WO200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 25.5%; Score 409; DB 5; Length 318;
Best Local Similarity 34.3%; Pred. No. 6.4e-25;
RESULT 782
ID ADJ67617 standard; protein; 351 AA.
DE Human ovarian specific polypeptide SEQ ID NO:331.
PN WO2004013311-A2.
PD 12-FEB-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 25.5%; Score 408.5; DB 8; Length 351;

Best Local Similarity 35.1%; Pred. No. 7.9e-25;
RESULT 783
ID AAY23321 standard; protein; 299 AA.
DE Amino acid sequence of the PRO301 polypeptide.
PN WO927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 2; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 784
ID AAW74464 standard; protein; 299 AA.
DE Fli antigen protein sequence.
PN WO902561-A1.
PD 21-JAN-1999.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 25.2%; Score 404; DB 2; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 785
ID AAY08071 standard; protein; 299 AA.
DE Human PRO307 protein.
PN WO914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 2; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 786
ID AAY13364 standard; protein; 299 AA.
DE Amino acid sequence of protein PRO301.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 2; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 787
ID AAY76011 standard; protein; 299 AA.
DE Human A33 receptor homologue, SEQ ID NO:189.
PN WO955865-A1.
PD 04-NOV-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 25.2%; Score 404; DB 3; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 788
ID AAY76076 standard; protein; 299 AA.
DE Human A33 receptor homologue, SEQ ID NO:331.
PN WO955865-A1.
PD 04-NOV-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 25.2%; Score 404; DB 3; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 789
ID AAY76070 standard; protein; 299 AA.
DE Human PRO301 protein.
PN WO200015797-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 3; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 790
ID AAB24405 standard; protein; 299 AA.
DE Human PRO301 protein sequence SEQ ID NO:90.
PN WO200032221-A2.
PD 08-JUN-2000.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 3; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 791
ID AAY95344 standard; protein; 299 AA.
DE Human PRO301 antitumour protein.
PN WO200037638-A2.
PD 29-JUN-2000.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 3; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 792
ID ADC78439 standard; protein; 299 AA.
DE Human PRO301 protein.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 3; Length 299;
Best Local Similarity 35.9%; Pred. No. 1.5e-24;
RESULT 793
ID AAB80232 standard; protein; 299 AA.
DE Human PRO301 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 4; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 794
ID AAM93577 standard; protein; 299 AA.
DE Human polypeptide, SEQ ID NO: 3365.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 25.2%; Score 404; DB 4; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 795
ID AAB56015 standard; protein; 299 AA.
DE Skin cell protein, SEQ ID NO: 331.
PN WO200069884-A2.
PD 23-NOV-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 25.2%; Score 404; DB 4; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 796
ID AAB55950 standard; protein; 299 AA.
DE Skin cell protein, SEQ ID NO: 189.
PN WO200069884-A2.
PD 23-NOV-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 25.2%; Score 404; DB 4; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 797
ID AAB31202 standard; protein; 299 AA.
DE Amino acid sequence of human polypeptide PRO301.
PN WO200077037-A2.
PD 21-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 4; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 798
ID AAU00823 standard; protein; 299 AA.
DE Human immune response protein PRO301 (UNQ264).
PN WO200119991-A1.
PD 22-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 4; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 799
ID AAU12354 standard; protein; 299 AA.
DE Human PRO301 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 4; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 800
ID AAB53086 standard; protein; 299 AA.
DE Human angiogenesis-associated protein PRO301, SEQ ID NO:119.
PN WO200053753-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 4; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 801

ID AAU14405 standard; protein; 299 AA.
DE Human novel protein #276.
PN WO200155437-A2.
PA (HUMA-) HUMAN GENOME SCI INC.
PD 02-AUG-2001.
Query Match 25.2%; Score 404; DB 4; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 802
ID AAU14404 standard; protein; 299 AA.
DE Human novel protein #275.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 25.2%; Score 404; DB 4; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 803
ID AAU14168 standard; protein; 299 AA.
DE Human novel protein #39.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 25.2%; Score 404; DB 4; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 804
ID AAU03896 standard; protein; 299 AA.
DE Human gene 23 encoded secreted protein fragment, SEQ ID NO:148.
PN WO200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 25.2%; Score 404; DB 4; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 805
ID AAU03840 standard; protein; 299 AA.
DE Human gene 23 encoded secreted protein HACAA29, SEQ ID NO: 86.
PN WO200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 25.2%; Score 404; DB 4; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 806
ID AAU03870 standard; protein; 299 AA.
DE Human gene 23 encoded secreted protein HACAA29, SEQ ID NO:116.
PN WO200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 25.2%; Score 404; DB 4; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 807
ID ABB90290 standard; protein; 299 AA.
DE Human polypeptide SEQ ID NO 2666.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 25.2%; Score 404; DB 5; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 808
ID ABB84843 standard; protein; 299 AA.
DE Human PRO301 protein sequence SEQ ID NO:54.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 5; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 809
ID ABB64551 standard; protein; 299 AA.
DE Human albumin fusion protein #1226.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 25.2%; Score 404; DB 5; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 810
ID ABB64552 standard; protein; 299 AA.
DE Human albumin fusion protein #1227.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 25.2%; Score 404; DB 5; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 811
ID ABB72215 standard; protein; 299 AA.
DE Human protein isolated from skin cells SEQ ID NO: 331.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 25.2%; Score 404; DB 5; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 812
ID ABB72150 standard; protein; 299 AA.
DE Human protein isolated from skin cells SEQ ID NO: 189.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 25.2%; Score 404; DB 5; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 813
ID ABB95449 standard; protein; 299 AA.
DE Human arginogenesis related protein PRO301 SEQ ID NO: 54.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 5; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 814
ID ABB71610 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 815
ID ABO17798 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 816
ID ABB71465 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 817
ID ABO25173 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003040014-A1.

PD 27-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 6; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 818
 ID ABU81052 standard; protein; 299 AA.
 DE Human PRO polypeptide #183.
 PN US2003004311-A1.
 PD 02-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 6; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 819
 ID ABU71911 standard; protein; 299 AA.
 DE Human secreted/transmembrane protein PRO301.
 PN US2003003530-A1.
 PD 02-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 6; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 820
 ID ABOU1794 standard; protein; 299 AA.
 DE Novel human secreted and transmembrane protein PRO301.
 PN US2002197671-A1.
 PD 26-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 6; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 821
 ID ABU66752 standard; protein; 299 AA.
 DE Human PRO polypeptide #183.
 PN US2003036180-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 6; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 822
 ID ABUS4367 standard; protein; 299 AA.
 DE Human secreted/transmembrane protein PRO301.
 PN US2002132240-A1.
 PD 19-SEP-2002.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 6; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 823
 ID ABU67291 standard; protein; 299 AA.
 DE Novel human secreted and transmembrane protein PRO301.
 PN US2003032063-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 6; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 824
 ID ABO47382 standard; protein; 299 AA.
 DE Human secreted/transmembrane polypeptide PRO301.
 PN US2003044839-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 6; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 825
 ID ABUS9833 standard; protein; 299 AA.
 DE Novel secreted and transmembrane protein PRO301.
 PN US2003017563-A1.
 PD 23-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 6; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 826
 ID ABO25023 standard; protein; 299 AA.
 DE Human secreted/transmembrane protein (PRO) #183.
 PN US2003036179-A1.
 PD 20-FEB-2003.

PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 6; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 827
 ID ABU64519 standard; protein; 299 AA.
 DE Human secreted/transmembrane protein, #23.
 PN US2002160374-A1.
 PD 31-OCT-2002.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 6; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 828
 ID ABU72059 standard; protein; 299 AA.
 DE Novel human secreted and transmembrane protein PRO301.
 PN US2002177165-A1.
 PD 28-NOV-2002.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 6; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 829
 ID ABU67365 standard; protein; 299 AA.
 DE Human secreted protein PRO301.
 PN US2003023054-A1.
 PD 30-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 6; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 830
 ID ABU67160 standard; protein; 299 AA.
 DE Novel human secreted and transmembrane protein PRO301.
 PN US2003032062-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 6; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 831
 ID ABO14885 standard; protein; 299 AA.
 DE Human secreted / transmembrane polypeptide PRO301.
 PN US2003036060-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 6; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 832
 ID ABU07736 standard; protein; 299 AA.
 DE Human A-33 related antigen PRO301.
 PN US2002182206-A1.
 PD 05-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 6; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 833
 ID AAO16451 standard; protein; 299 AA.
 DE Human junctional adhesion molecule 1 (huJAM1).
 PN WO2003008541-A2.
 PD 30-JAN-2003.
 PA (ELIL) LILLY & CO ELI.
 Query Match 25.2%; Score 404; DB 6; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 834
 ID ABU67028 standard; protein; 299 AA.
 DE Human secreted/transmembrane, PRO, protein SEQ ID 366.
 PN US2003032155-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 6; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 835
 ID ABU69642 standard; protein; 299 AA.
 DE Novel human secreted and transmembrane protein PRO301.
 PN US2003017463-A1.
 PD 23-JAN-2003.
 PA (GETH) GENENTECH INC.

Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 836
ID ABU79802 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO301.
PN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 837
ID ABO14824 standard; protein; 299 AA.
DE Human secreted / transmembrane polypeptide PRO301.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 838
ID ADA45885 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 839
ID ADA76316 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 840
ID ADB29324 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 841
ID ADA18966 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 842
ID ADA61589 standard; protein; 299 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 843
ID ADB19374 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 844
ID ADB27915 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;

Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 845
ID ADA86394 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 846
ID ADB15958 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 847
ID ADA47744 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 848
ID ADA18180 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 849
ID ABO32776 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO301.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 850
ID ADA67539 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 851
ID ADB30546 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 852
ID ADA85842 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 853
ID ADA97054 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;

RESULT 854
ID ADA79358 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 855
ID ADA87497 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 856
ID ADB16699 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 857
ID ABO34836 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 858
ID ADA16155 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 859
ID ADA91791 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 860
ID ADB14854 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 861
ID ADA47263 standard; protein; 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.
PN US2003044844-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 862
ID ADB18815 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 863
ID ADA85290 standard; protein; 299 AA.

ID ADA94030 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 864
ID ADB19926 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 865
ID ADB13238 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 866
ID ABO43331 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 867
ID ADA74492 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 868
ID ADA42300 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 869
ID ADB24725 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 870
ID ADA82249 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 871
ID ADA75212 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 872
ID ADA85290 standard; protein; 299 AA.

DE Novel human secreted and transmembrane protein PRO301.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 873
ID ADA84738 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 874
ID ABO17514 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 875
ID ADB29994 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 876
ID ADA80522 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 877
ID ADA75764 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 878
ID ADA46989 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 879
ID ADB25285 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 880
ID ADA93461 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 881
ID ADB26811 standard; protein; 299 AA.
DE Human PRO polypeptide #183.

PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 882
ID ADB31098 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 883
ID ADA61026 standard; protein; 299 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 884
ID ADB24173 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 885
ID ADA96502 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 886
ID ADA81074 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 887
ID ADA95950 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 888
ID ADB26259 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 889
ID ADB21744 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 890
ID ADA77523 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003068797-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 891
ID ADB18263 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US200307710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 892
ID ADA66946 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 893
ID ADA16579 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US200303969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 894
ID ADA13008 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 895
ID ADA1876 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 896
ID ADA88049 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 897
ID ADA46437 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 898
ID ADA17223 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 899
ID ADA42726 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003054351-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 900
ID ADB28467 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 901
ID ADB29019 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 902
ID ADA76971 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 903
ID ADA88601 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 904
ID ADA97606 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 905
ID ADB27363 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 906
ID ADB22296 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 907
ID ABO19860 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO302.
PN US2003044902-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 908
ID ABO17575 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;

RESULT 909
ID ADA66987 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
FN US2003068793-A1.
PD 10-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 910
ID ADB22848 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
FN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 911
ID ADB23621 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
FN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 912
ID ADA92343 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
FN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 913
ID ADB15406 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
FN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 914
ID ADB38658 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
FN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 915
ID ADB38106 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
FN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 916
ID ADB66578 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
FN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 917
ID ADB89658 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
FN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 918
ID ADB33931 standard; protein; 299 AA.

ID ADB90390 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
FN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 919
ID ADB77645 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
FN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 920
ID ADB39491 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
FN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 921
ID ADB74781 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
FN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 922
ID ADB47114 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
FN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 923
ID ADB6721 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
FN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 924
ID ADB77326 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
FN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 925
ID ADB34483 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
FN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 926
ID ADB3587 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
FN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 927
ID ADB33931 standard; protein; 299 AA.

DE Human PRO polypeptide SEQ ID NO 366.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 928
ID ADB35035 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 929
ID ADB36139 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 930
ID ADB46534 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 931
ID ADC28427 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 932
ID ADC39627 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 933
ID ADC40141 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 934
ID ADC18969 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 935
ID ADC34265 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 936
ID ADC29320 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.

PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 937
ID ADC28851 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 938
ID ADC40736 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 939
ID ADC19393 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 940
ID ADC33841 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 941
ID ADC12911 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 942
ID ADC50407 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 943
ID ADC71954 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 944
ID ADC59933 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 945
ID ADC52940 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US2003087365-A1.

PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 946
ID ADC57294 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 947
ID ADC60485 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 948
ID ADC50960 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 949
ID ADC65487 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 950
ID ADC5485 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 951
ID ADC53546 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 952
ID ADC59069 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 953
ID ADC55947 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 954
ID ADC58517 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US2003087346-A1.
PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 955
ID ADC12363 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 956
ID ADD03191 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 957
ID ADC90183 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 958
ID ADC69602 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 959
ID ADC48491 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 960
ID ADD10020 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 961
ID ADD04595 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 962
ID ADC80551 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 963
ID ADD11058 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 964
ID ADD10343 standard; protein; 299 AA.
DE Human secreted/transmembrane PRO polypeptide #27.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 965
ID ADC47939 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 966
ID ADD04918 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 967
ID ADC79999 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 968
ID ADD11303 standard; protein; 299 AA.
DE Human secreted/transmembrane PRO polypeptide #27.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 969
ID ADD09468 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 970
ID ADD03924 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 971
ID ADD03500 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 972
ID ADD41181 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;

Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 973
ID ADD52320 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 974
ID ADD53060 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 975
ID ADD53612 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 976
ID ADD37096 standard; protein; 299 AA.
DE Human secreted/transmembrane PRO polypeptide #27.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 977
ID ADD51768 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 978
ID ADD02567 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 979
ID ADD02001 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 980
ID ADD54183 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 981
ID ADD92500 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;

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RESULT 982
ID ADE91396 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 983
ID ADE04010 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 984
ID ADE32307 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 985
ID ADE22239 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 986
ID ADE79463 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 987
ID ADE41999 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 988
ID ADE17816 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 989
ID ADD91948 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 990
ID ADE33411 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 991
ID ADE33963 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 992
ID ADD80015 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 993
ID ADD93052 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 994
ID ADE19472 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 995
ID ADE34752 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 996
ID ADE18920 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 997
ID ADE43116 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 998
ID ADD95905 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 999
ID ADE22791 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1000
ID ADD78909 standard; protein; 299 AA.
```

DE Human PRO polypeptide #183.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1001
ID ADE32859 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1002
ID ADE42551 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1003
ID ADD80567 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1004
ID ADD89595 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1005
ID ADE40879 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1006
ID ADE04678 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1007
ID ADE92807 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1008
ID ADG21516 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1009
ID ADG23157 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.

PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1010
ID ADF97492 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1011
ID ADG80556 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1012
ID ADG80004 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1013
ID ADG63772 standard; protein; 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.
PN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1014
ID ADH62528 standard; protein; 299 AA.
DE Human PRO301 protein.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1015
ID ADH59235 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1016
ID ADH55296 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1017
ID ADH55848 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1018
ID ADI38014 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1019
ID ADI64067 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1020
ID ADI65016 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1021
ID ADI63515 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1022
ID ADH81929 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1023
ID ADH81377 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1024
ID ADJ26282 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1025
ID ADM82546 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1026
ID ADNI5945 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;

Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1027
ID ADNI6574 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1028
ID ADNI5393 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1029
ID ADNI4841 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1030
ID ADC81103 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1031
ID ADE79197 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1032
ID ADD76551 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1033
ID ADD87915 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1034
ID ADD86319 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1035
ID ADE79621 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;

RESULT 1036
ID ADE75767 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #183.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1037
ID ADE73297 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1038
ID ADE41304 standard; protein; 299 AA.
DE Human secreted/transmembrane PRO polypeptide #27.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1039
ID ADE23343 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1040
ID ADE23895 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1041
ID ADE24538 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1042
ID ADD87363 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1043
ID ADE89229 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1044
ID ADE41186 standard; protein; 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.
PN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1045
ID ADE98505 standard; protein; 299AA.
DE Human secreted/transmembrane protein, #25.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1046
ID ADE18368 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1047
ID ADE88677 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1048
ID ADE99386 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1049
ID ADE94697 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1050
ID ADE91108 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1051
ID ADE95249 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1052
ID ADE93359 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1053
ID ADF34940 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;

DE Human secreted/transmembrane protein, #25.
 PN US2003211569-A1.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 8; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 1063
 ID ADG20138 standard; protein; 299 AA.
 DE Human PRO polypeptide #183.
 PN US2003207376-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 8; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 1064
 ID ADF98044 standard; protein; 299 AA.
 DE Human PRO polypeptide #183.
 PN US2003207422-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 8; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 1065
 ID ADG24261 standard; protein; 299 AA.
 DE Novel human secreted and transmembrane protein PRO301.
 PN US2003207426-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 8; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 1066
 ID ADF98615 standard; protein; 299 AA.
 DE Human PRO polypeptide #183.
 PN US2003208055-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 8; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 1067
 ID ADG03446 standard; protein; 299 AA.
 DE Human PRO polypeptide #183.
 PN US2003207351-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 8; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 1068
 ID ADF99167 standard; protein; 299 AA.
 DE Human PRO polypeptide #183.
 PN US2003207353-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 8; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 1069
 ID ADG16752 standard; protein; 299 AA.
 DE Human PRO polypeptide #183.
 PN US2003207359-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 8; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 1070
 ID ADG05211 standard; protein; 299 AA.
 DE Human PRO polypeptide #183.
 PN US2003207375-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 8; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 1071
 ID ADG19478 standard; protein; 299 AA.
 DE Human PRO polypeptide #183.
 PN US2003207425-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.

DE Human secreted/transmembrane protein, #25.
 PN US2003211569-A1.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 8; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 1055
 ID ADE92255 standard; protein; 299 AA.
 DE Novel human secreted and transmembrane protein PRO301.
 PN US2003199051-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 8; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 1056
 ID ADE90556 standard; protein; 299 AA.
 DE Human PRO polypeptide #183.
 PN US2003199063-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 8; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 1057
 ID ADE91703 standard; protein; 299 AA.
 DE Novel human secreted and transmembrane protein PRO301.
 PN US2003199058-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 8; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 1058
 ID ADE98932 standard; protein; 299 AA.
 DE Human secreted/transmembrane protein, #25.
 PN US2003211568-A1.
 PD 13-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 8; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 1059
 ID ADG40402 standard; protein; 299 AA.
 DE Human secreted/transmembrane protein, #25.
 PN US2003225253-A1.
 PD 04-DEC-2003.
 PA (DESN/) DESNOYERS L.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (MATH/) MATHIER J P.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Query Match 25.2%; Score 404; DB 8; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 1060
 ID ADF73796 standard; protein; 299 AA.
 DE Human secreted/transmembrane protein, #25.
 PN US2003180312-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 8; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 1061
 ID AGO2282 standard; protein; 299 AA.
 DE Human PRO polypeptide #183.
 PN US2003207352-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 8; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 1062
 ID ADG22068 standard; protein; 299 AA.
 DE Novel human secreted and transmembrane protein PRO301.
 PN US2003207360-A1.
 PD 06-NOV-2003.

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Query Match      25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1072
ID ADF7372 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1073
ID ADG13315 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1074
ID ADG08372 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1075
ID ADG15542 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1076
ID ADP6940 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1077
ID ADG06125 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1078
ID ADG23709 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1079
ID ADG03998 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1080
ID ADG24899 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1081
ID ADG07196 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1082
ID ADG07748 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1083
ID ADG55243 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1084
ID ADG60907 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1085
ID ADG62011 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1086
ID ADG92215 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1087
ID ADG82212 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1088
ID ADG57451 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1089
ID ADG56899 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
```


RESULT 1090
ID ADG5795 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1091
ID ADG5855 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1092
ID ADG70921 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1093
ID ADG92642 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1094
ID ADG58003 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1095
ID ADG53587 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1096
ID ADG71473 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1097
ID ADG81660 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1098
ID ADH30622 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1099
ID ADG63621 standard; protein; 299 AA.

DE Human secreted/transmembrane polypeptide PRO301.
PN US2003180796-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1100
ID ADH11989 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1101
ID ADG52411 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1102
ID ADG54139 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1103
ID ADG81108 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1104
ID ADG56347 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1105
ID ADH12613 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1106
ID ADG61459 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1107
ID ADH28546 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1108
ID ADG54691 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.

PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1109
ID ADG59731 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1110
ID ADH20431 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1111
ID ADH43487 standard; protein; 299 AA.
DE Human PRO polypeptide #27.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1112
ID ADH07286 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOVERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1113
ID ADH59831 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1114
ID ADH06859 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOVERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1115
ID ADI18155 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1116
ID ADI18601 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1117
ID ADI65321 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1118
ID ADI37584 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1119
ID ADG09898 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1120
ID ADH97380 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1121
ID ADI15369 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1122
ID ADG09246 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1123
ID ADI65748 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1124
ID ADI14701 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1125

ID ADH60491 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PD US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOVERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHIER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1126
ID ADI18296 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PD US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1127
ID ADJ95548 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PD US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1128
ID ADL08741 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PD US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1129
ID ADI47176 standard; protein; 299 AA.
DE Human JAM-1 protein sequence.
PD WO2004003145-A2.
PD 08-JAN-2004.
PA (NAST-) NASTECH PHARM CO INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1130
ID ADM25082 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PD US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1131
ID ADK40844 standard; protein; 299 AA.
DE Human platelet F11 receptor #1.
PD US669688-B1.
PD 02-MAR-2004.
PA (UNY) UNIV NEW YORK STATE RES FOUND.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1132
ID ADJ63577 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PD US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1133
ID ADM29832 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PD US2003190611-A1.

PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1134
ID ADL77818 standard; protein; 299 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 1300.
PD US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1135
ID ADL77819 standard; protein; 299 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 1301.
PD US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1136
ID ADJ77472 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PD US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1137
ID ADK82832 standard; protein; 299 AA.
DE Human PRO polypeptide #27.
PD US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1138
ID ADJ65594 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PD US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1139
ID ADL31332 standard; protein; 299 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3365.
PD EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1140
ID ADM27730 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PD US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1141
ID ADL26800 standard; protein; 299 AA.
DE Human JAM1 protein SEQ ID NO:54.
PD WO2004022778-A1.
PD 18-MAR-2004.
PA (GARV-) GARVAN INST MEDICAL RES.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1142
ID ADM42454 standard; protein; 299 AA.
DE Human PRO polypeptide #183.

PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1143
ID ADO06154 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1144
ID ADN35284 standard; protein; 299 AA.
DE Human PRO301 protein.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1145
ID ADN05140 standard; protein; 299 AA.
DE Antipsoriatic protein sequence #749.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1146
ID ADM28316 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1147
ID ADQ95890 standard; protein; 299 AA.
DE T cell activation associated protein #34.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAHI) ASAHI KASEI PHARMA CORP.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1148
ID ADRI1006 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1149
ID ADRI7915 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK) ASHKENAZI A.
PA (BOTS) BOTSTEIN D.
PA (DESN) DESNOYERS L.
PA (EATO) EATON D L.
PA (FERR) FERRARA N.
PA (FILV) FILVAROFF E.
PA (FONG) FONG S.
PA (GAOW) GAO W.
PA (GERB) GERBER H.
PA (GERR) GERRITSEN M E.
PA (GODD) GODDARD A.
PA (GODO) GODOWSKI P J.
PA (GRIM) GRIMALDI C J.
PA (GURN) GURNEY A L.
PA (HILL) HILLAN K J.

PA (KLJA) KLJAVIN I J.
PA (MATH) MATHER J P.
PA (PANJ) PAN J.
PA (PAON) PAONI N F.
PA (ROYM) ROY M A.
PA (STEW) STEWART T A.
PA (TUNA) TUNAS D.
PA (WILL) WILLIAMS P M.
PA (WOOD) WOOD W I.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1150
ID ADR27641 standard; protein; 299 AA.
DE Human F11 receptor protein Seq 7.
PN WO2004063327-A2.
PD 29-JUL-2004.
PA (KORN) KORNECKI E.
PA (BABI) BABINSKA A.
PA (EHR) EHRlich Y H.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1151
ID ADI95798 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1152
ID ADI96350 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1153
ID ADR46577 standard; protein; 299 AA.
DE Human JAM-1, F11 receptor (F11R) transcript variant 4, SEQ ID 8.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (DOKU) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1154
ID ADR46571 standard; protein; 299 AA.
DE Human JAM-1, F11 receptor (F11R) transcript variant 4.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (DOKU) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1155
ID ADR46573 standard; protein; 299 AA.
DE Human JAM-1, F11 receptor (F11R) transcript variant 4.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (DOKU) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1156
ID ADR46579 standard; protein; 299 AA.
DE Human JAM-1, F11 receptor (F11R) transcript variant 5.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (DOKU) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1157
ID ADT94260 standard; protein; 299 AA.
DE Human PRO301 protein.
PN AU2003259607-A1.

PD 27-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 8; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 1158
 ID ADS74554 standard; protein; 299 AA.
 DE Human secreted/transmembrane protein #25.
 PN US200418531-A1.
 PD 23-SEP-2004.
 PA (ASHK/) ASHKENAZI A.
 PA (BOTS/) BOTSTEIN D.
 PA (DESN/) DESNOYERS L.
 PA (EATO/) EATON D L.
 PA (FERR/) FERRARA N.
 PA (FILV/) FILVAROFF E.
 PA (FONG/) FONG S.
 PA (GAOW/) GAO W.
 PA (GERE/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GRIM/) GRIMALDI C J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (KLJA/) KLJAVIN I J.
 PA (MATH/) MATHER J P.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (ROYM/) ROY M A.
 PA (STEW/) STEWART T A.
 PA (TUMA/) TUMAS D.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Query Match 25.2%; Score 404; DB 8; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 1159
 ID ADS32302 standard; protein; 299 AA.
 DE Novel human secreted and transmembrane protein PRO301.
 PN US2004203125-A1.
 PD 14-OCT-2004.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 8; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 1160
 ID ADT03286 standard; protein; 299 AA.
 DE Human PRO polypeptide #183.
 PN US2004214269-A1.
 PD 28-OCT-2004.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 8; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 1161
 ID ADT03591 standard; protein; 299 AA.
 DE Human secreted/transmembrane protein, #25.
 PN US2003152922-A1.
 PD 14-AUG-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 8; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 1162
 ID ADU06480 standard; protein; 299 AA.
 DE Novel bronchial cancer-associated human protein SeqID704.
 PN DE10316701-A1.
 PD 04-NOV-2004.
 PA (HINZ/) HINZMANN B.
 PA (HERM/) HERMANN K.
 PA (CAST/) HEIDEN CASTANOS-VELEZ E.
 Query Match 25.2%; Score 404; DB 8; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 1163
 ID ADU06355 standard; protein; 299 AA.
 DE Novel bronchial cancer-associated human protein SeqID579.
 PN DE10316701-A1.

PD 04-NOV-2004.
 PA (HINZ/) HINZMANN B.
 PA (HERM/) HERMANN K.
 PA (CAST/) HEIDEN CASTANOS-VELEZ E.
 Query Match 25.2%; Score 404; DB 8; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 1164
 ID ADU66684 standard; protein; 299 AA.
 DE Human platelet FII receptor protein, FIIIR-A.
 PN US2004235768-A1.
 PD 25-NOV-2004.
 PA (KORV/) KORNECKI E.
 PA (SOBO/) SOBOCKA M B.
 Query Match 25.2%; Score 404; DB 8; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 1165
 ID ADW97860 standard; protein; 299 AA.
 DE Human junctional adhesion molecule-1 (JAM-1) protein.
 PN US2005025776-A1.
 PD 03-FEB-2005.
 PA (WEBE/) WEBER C.
 Query Match 25.2%; Score 404; DB 9; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 1166
 ID ADZ03337 standard; protein; 299 AA.
 DE Human secreted/transmembrane PRO301 protein.
 PN US2005074837-A1.
 PD 07-APR-2005.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 9; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 1167
 ID AEA37829 standard; protein; 299 AA.
 DE Human secreted/transmembrane protein, #25.
 PN US2005112725-A1.
 PD 26-MAY-2005.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 9; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 1168
 ID AEA29245 standard; protein; 299 AA.
 DE Human junction adhesion molecule -1 as target for drug delivery method.
 PN US2005129679-A1.
 PD 16-JUN-2005.
 PA (NAST-) NASTECH PHARM CO INC.
 Query Match 25.2%; Score 404; DB 9; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 1169
 ID AEB14083 standard; protein; 299 AA.
 DE Cancer cell diagnosis method-related human protein - SEQ ID 366.
 PN US2005153396-A1.
 PD 14-JUL-2005.
 PA (BAKE/) BAKER K P.
 PA (BERE/) BERESINI M.
 PA (DEFO/) DEFORGE L.
 PA (DESN/) DESNOYERS L.
 PA (FILV/) FILVAROFF E.
 PA (GAOW/) GAO W.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (SHER/) SHERWOOD S.
 PA (SMIT/) SMITH V.
 PA (STEW/) STEWART T A.
 PA (TUMA/) TUMAS D.
 PA (WATA/) WATANABE C K.
 PA (WOOD/) WOOD W I.
 PA (ZHAN/) ZHANG Z.
 Query Match 25.2%; Score 404; DB 9; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.5e-24;
 RESULT 1170
 ID AED23863 standard; protein; 299 AA.

DE Human secreted protein PRO 301, SEQ ID 119.
PN US2005214904-A1.
PD 29-SEP-2005.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 9; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1171
ID AED86281 standard; protein; 299 AA.
DE Human PRO amino acid sequence, seq id 366.
PN US2005245730-A1.
PD 03-NOV-2005.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 9; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1172
ID AEE24079 standard; protein; 299 AA.
DE Novel human protein amino acid sequence - SEQ ID 748.
PN US2005266423-A1.
PD 01-DEC-2005.
PA (NUVE-) NUVELO INC.
Query Match 25.2%; Score 404; DB 10; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1173
ID AEE24078 standard; protein; 299 AA.
DE Novel human protein amino acid sequence - SEQ ID 747.
PN US2005266423-A1.
PD 01-DEC-2005.
PA (NUVE-) NUVELO INC.
Query Match 25.2%; Score 404; DB 10; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1174
ID AEE23606 standard; protein; 299 AA.
DE Novel human protein amino acid sequence - SEQ ID 275.
PN US2005266423-A1.
PD 01-DEC-2005.
PA (NUVE-) NUVELO INC.
Query Match 25.2%; Score 404; DB 10; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1175
ID AEE69032 standard; protein; 299 AA.
DE Cancer associated antigen homologous PRO301 protein, SEQ ID 119.
PN US6974689-B1.
PD 13-DEC-2005.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 10; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1176
ID AEG58228 standard; protein; 299 AA.
DE Human PRO301 polypeptide SEQ ID NO: 366.
PN US2006073568-A1.
PD 06-APR-2006.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 10; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1177
ID AEH08093 standard; protein; 299 AA.
DE Therapeutic protein HACAA29, SEQ ID 1301.
PN US2006084794-A1.
PD 20-APR-2006.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 25.2%; Score 404; DB 10; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1178
ID AEH08092 standard; protein; 299 AA.
DE Therapeutic protein HACAA29, SEQ ID 1300.
PN US2006084794-A1.
PD 20-APR-2006.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 25.2%; Score 404; DB 10; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1179
ID AEI43873 standard; protein; 299 AA.
DE Human cancer-related PRO protein amino acid sequence - SEQ ID 366.
PN US2006040351-A1.
PD 23-FEB-2006.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFORGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match 25.2%; Score 404; DB 10; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1180
ID AEI23956 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO301, SEQ ID NO:366.
PN EP1672070-A2.
PD 21-JUN-2006.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 10; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1181
ID AEL49650 standard; protein; 299 AA.
DE Human PRO301 protein, SEQ ID NO: 1.
PN US2006233803-A1.
PD 19-OCT-2006.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 10; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1182
ID ADE09073 standard; protein; 320 AA.
DE Novel protein-related contig polypeptide sequence #139.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 25.2%; Score 404; DB 7; Length 320;
Best Local Similarity 35.2%; Pred. No. 1.6e-24;
RESULT 1183
ID ADU40591 standard; protein; 320 AA.
DE Novel human polypeptide seq id 376.
PN US2004219521-A1.
PD 04-NOV-2004.
PA (TANG/) TANG Y T.
PA (WANG/) WANG Z.
PA (WENG/) WENG G.
PA (BOYL/) BOYLE B J.
PA (DRMA/) DRMANAC R T.
Query Match 25.2%; Score 404; DB 9; Length 320;
Best Local Similarity 35.2%; Pred. No. 1.6e-24;
RESULT 1184
ID ADE08038 standard; protein; 336 AA.
DE Novel protein (useful for identifying genetic disorders) #193.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 25.2%; Score 404; DB 7; Length 336;
Best Local Similarity 35.2%; Pred. No. 1.8e-24;
RESULT 1185
ID ADU40408 standard; protein; 336 AA.
DE Novel human polypeptide seq id 193.
PN US2004219521-A1.
PD 04-NOV-2004.
PA (TANG/) TANG Y T.
PA (WANG/) WANG Z.
PA (WENG/) WENG G.

PA (BOYLE/) BOYLE B J.
PA (DRMA/) DRMANAC R T.
Query Match 25.0%; Score 404; DB 9; Length 336;
Best Local Similarity 35.2%; Pred. No. 1.8e-24;
RESULT 1186
ID AAY23326 standard; protein; 260 AA.
DE An A33 related antigen sequence.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match 25.0%; Score 401; DB 2; Length 260;
Best Local Similarity 38.4%; Pred. No. 2.2e-24;
RESULT 1187
ID AAY08072 standard; protein; 260 AA.
DE Human DNA40628 protein.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 25.0%; Score 401; DB 2; Length 260;
Best Local Similarity 38.4%; Pred. No. 2.2e-24;
RESULT 1188
ID ADH62550 standard; protein; 260 AA.
DE Human PRO301 protein fragment #1.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 25.0%; Score 401; DB 7; Length 260;
Best Local Similarity 38.4%; Pred. No. 2.2e-24;
RESULT 1189
ID AEL49672 standard; protein; 260 AA.
DE Human PRO301 fragment, residues 24-283, SEQ ID NO: 23.
PN US2006233803-A1.
PD 19-OCT-2006.
PA (GETH) GENENTECH INC.
Query Match 25.0%; Score 401; DB 10; Length 260;
Best Local Similarity 38.4%; Pred. No. 2.2e-24;
RESULT 1190
ID AAY23328 standard; protein; 263 AA.
DE An A33 related antigen sequence.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match 25.0%; Score 401; DB 2; Length 263;
Best Local Similarity 38.4%; Pred. No. 2.3e-24;
RESULT 1191
ID AAY08074 standard; protein; 263 AA.
DE Human DNA40628 protein fragment #2.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 25.0%; Score 401; DB 2; Length 263;
Best Local Similarity 38.4%; Pred. No. 2.3e-24;
RESULT 1192
ID ADH62552 standard; protein; 263 AA.
DE Human PRO301 protein fragment #2.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 25.0%; Score 401; DB 7; Length 263;
Best Local Similarity 38.4%; Pred. No. 2.3e-24;
RESULT 1193

ID AEL49674 standard; protein; 263 AA.
DE Human PRO301 fragment, residues 21-239, SEQ ID NO: 25.
PN US2006233803-A1.
PD 19-OCT-2006.
PA (GETH) GENENTECH INC.
Query Match 25.0%; Score 401; DB 10; Length 263;
Best Local Similarity 38.4%; Pred. No. 2.3e-24;
RESULT 1194
ID ADJ67616 standard; protein; 335 AA.
DE Human ovarian specific polypeptide SEQ ID NO:330.
PN WO2004013311-A2.
PD 12-FEB-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 24.6%; Score 395; DB 8; Length 335;
Best Local Similarity 35.7%; Pred. No. 9.5e-24;
RESULT 1195
ID AAW61380 standard; protein; 300 AA.
DE Mouse junctional adhesion molecule protein.
PN WO9824897-A1.
PD 11-JUN-1998.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 24.5%; Score 394; DB 2; Length 300;
Best Local Similarity 34.8%; Pred. No. 1e-23;
RESULT 1196
ID AAY23325 standard; protein; 300 AA.
DE A33 related antigen JAM.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match 24.5%; Score 394; DB 2; Length 300;
Best Local Similarity 34.8%; Pred. No. 1e-23;
RESULT 1197
ID ADH62537 standard; protein; 300 AA.
DE Murine JAM protein used in the exemplification of the invention.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 24.5%; Score 394; DB 7; Length 300;
Best Local Similarity 34.8%; Pred. No. 1e-23;
RESULT 1198
ID ADK40853 standard; protein; 300 AA.
DE Mouse junction adhesion molecule (JAM).
PN US6699688-B1.
PD 02-MAR-2004.
PA (UTNY) UNIV NEW YORK STATE RES FOUND.
Query Match 24.5%; Score 394; DB 8; Length 300;
Best Local Similarity 34.8%; Pred. No. 1e-23;
RESULT 1199
ID ADN35293 standard; protein; 300 AA.
DE Human JAM protein.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 24.5%; Score 394; DB 8; Length 300;
Best Local Similarity 34.8%; Pred. No. 1e-23;
RESULT 1200
ID ADR46581 standard; protein; 300 AA.
DE Mouse junctional adhesion molecule-1, SEQ ID 12.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSHI HOJIN KAGAKU GIJUTSU SH.
Query Match 24.5%; Score 394; DB 8; Length 300;
Best Local Similarity 34.8%; Pred. No. 1e-23;
RESULT 1201
ID ADU66693 standard; protein; 300 AA.
DE Mouse junctional adhesion molecule (JAM).
PN US2004235768-A1.

PD 25-NOV-2004.
PA (KORN/) KORNECKI E.
PA (SOBO/) SOBOCKA M B.
Query Match 24.5%; Score 394; DB 8; Length 300;
Best Local Similarity 34.8%; Pred. No. 1e-23;
RESULT 1202
ID AEL4959 standard; protein; 300 AA.
DE Human junctional adhesion molecule, SEQ ID NO: 10.
PN US2006233803-A1.
PD 19-OCT-2006.
PA (GETH) GENENTECH INC.
Query Match 24.5%; Score 394; DB 10; Length 300;
Best Local Similarity 34.8%; Pred. No. 1e-23;
RESULT 1203
ID ADH80723 standard; protein; 300 AA.
DE Human polypeptide #40.
PN US2003232054-A1.
PD 18-DEC-2003.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (CHEN/) CHEN R.
PA (QIAN/) QIAN X B.
PA (WANG/) WANG Z W.
PA (WEHR/) WEHRMAN T.
PA (ZHAN/) ZHANG J.
PA (ZHOU/) ZHOU P.
PA (CAOY/) CAO Y.
PA (DRNA/) DRMANAC R T.
Query Match 24.5%; Score 392.5; DB 8; Length 300;
Best Local Similarity 35.1%; Pred. No. 1.3e-23;
RESULT 1204
ID ADH80722 standard; protein; 301 AA.
DE Human polypeptide #39.
PN US2003232054-A1.
PD 18-DEC-2003.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (CHEN/) CHEN R.
PA (QIAN/) QIAN X B.
PA (WANG/) WANG Z W.
PA (WEHR/) WEHRMAN T.
PA (ZHAN/) ZHANG J.
PA (ZHOU/) ZHOU P.
PA (CAOY/) CAO Y.
PA (DRNA/) DRMANAC R T.
Query Match 24.0%; Score 385; DB 8; Length 301;
Best Local Similarity 34.9%; Pred. No. 5.5e-23;
RESULT 1205
ID AAB39253 standard; protein; 280 AA.
DE Gene 15 human secreted protein homologous amino acid sequence #133.
PN WO200056754-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.9%; Score 383; DB 3; Length 280;
Best Local Similarity 36.2%; Pred. No. 7.3e-23;
RESULT 1206
ID ADQ95892 standard; protein; 259 AA.
DE T cell activation associated protein #35.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match 23.2%; Score 372.5; DB 8; Length 259;
Best Local Similarity 37.3%; Pred. No. 4.8e-22;
RESULT 1207
ID ADR46575 standard; protein; 259 AA.
DE Human JAM-1, F11 receptor (F11R) transcript variant 3.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Query Match 23.2%; Score 372.5; DB 8; Length 259;
Best Local Similarity 37.3%; Pred. No. 4.8e-22;

RESULT 1208
ID AAUI4169 standard; protein; 259 AA.
DE Human novel protein #40.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 22.8%; Score 366.5; DB 4; Length 259;
Best Local Similarity 36.8%; Pred. No. 1.5e-21;
RESULT 1209
ID AEE23607 standard; protein; 259 AA.
DE Novel human protein amino acid sequence - SEQ ID 276.
PN US2005266423-A1.
PD 01-DEC-2005.
PA (NUVE-) NUVELO INC.
Query Match 22.8%; Score 366.5; DB 10; Length 259;
Best Local Similarity 36.8%; Pred. No. 1.5e-21;
RESULT 1210
ID ADF12431 standard; protein; 238 AA.
DE Human adhesion molecule JAM-2.
PN WO2003087128-A2.
PD 23-OCT-2003.
PA (RMFD-) RMF DICTAGENE SA.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 22.8%; Score 365.5; DB 7; Length 238;
Best Local Similarity 34.7%; Pred. No. 1.6e-21;
RESULT 1211
ID ADG39449 standard; protein; 238 AA.
DE Human JAM-2 protein SEQ ID NO:18.
PN WO2003104400-A2.
PD 18-DEC-2003.
PA (RMFD-) RMF DICTAGENE SA.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 22.8%; Score 365.5; DB 8; Length 238;
Best Local Similarity 34.7%; Pred. No. 1.6e-21;
RESULT 1212
ID ADP56685 standard; protein; 265 AA.
DE Human junction adhesion molecule 3 splice variant 2 (huJAM3sv2) protein.
PN WO2004053058-A2.
PD 24-JUN-2004.
PA (ELIL) LILLY & CO ELI.
Query Match 22.8%; Score 365.5; DB 8; Length 265;
Best Local Similarity 34.7%; Pred. No. 1.8e-21;
RESULT 1213
ID ADU06841 standard; protein; 265 AA.
DE Cell adhesion and extracellular matrix protein clone 7518734CD1.
PN WO2004094623-A2.
PD 04-NOV-2004.
PA (INCY-) INCYTE CORP.
Query Match 22.8%; Score 365.5; DB 8; Length 265;
Best Local Similarity 34.7%; Pred. No. 1.8e-21;
RESULT 1214
ID ABG22339 standard; protein; 69 AA.
DE Novel human diagnostic protein #22330.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 22.2%; Score 357; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.6e-21;
RESULT 1215
ID ADP69098 standard; protein; 206 AA.
DE Human NOV2a mature extracellular domain protein SEQ ID NO:68.
PN WO2004055158-A2.
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match 22.2%; Score 357; DB 8; Length 206;
Best Local Similarity 36.8%; Pred. No. 6.6e-21;
RESULT 1216
ID ADP69031 standard; protein; 206 AA.
DE Human NOV2d protein SEQ ID NO:26.
PN WO2004055158-A2.
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match 22.2%; Score 357; DB 8; Length 206;

Best Local Similarity 36.8%; Pred. No. 6.6e-21;
RESULT 1217
ID ADP69029 standard; protein; 206 AA.
DE Human NOV2c protein SEQ ID NO:24.
PN WO2004055158-A2.
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match 22.2%; Score 357; DB 8; Length 206;
Best Local Similarity 36.8%; Pred. No. 6.6e-21;
RESULT 1218
ID AAW61379 standard; protein; 298 AA.
DE Human junctional adhesion molecule protein.
PN WO9824897-A1.
PD 11-JUN-1998.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 21.5%; Score 344.5; DB 2; Length 298;
Best Local Similarity 31.8%; Pred. No. 1.1e-19;
RESULT 1219
ID ADQ56575 standard; protein; 259 AA.
DE Novel human protein sequence #648.
PN EF1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 21.4%; Score 344; DB 8; Length 259;
Best Local Similarity 30.1%; Pred. No. 1e-19;
RESULT 1220
ID ABG22401 standard; protein; 361 AA.
DE Novel human diagnostic protein #22392.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 21.2%; Score 341; DB 4; Length 361;
Best Local Similarity 30.0%; Pred. No. 2.8e-19;
RESULT 1221
ID ABG12109 standard; protein; 404 AA.
DE Novel human diagnostic protein #12100.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 19.0%; Score 304.5; DB 4; Length 404;
Best Local Similarity 27.1%; Pred. No. 3.2e-16;
RESULT 1222
ID ABG04645 standard; protein; 291 AA.
DE Novel human diagnostic protein #4636.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 18.9%; Score 303.5; DB 4; Length 291;
Best Local Similarity 29.6%; Pred. No. 2.5e-16;
RESULT 1223
ID ADP56684 standard; protein; 229 AA.
DE Human junction adhesion molecule 3 splice variant 1 (huJAM3sv1) protein.
PN WO2004053058-A2.
PD 24-JUN-2004.
PA (ELIL) LILLY & CO ELI.
Query Match 18.7%; Score 300.5; DB 8; Length 229;
Best Local Similarity 33.0%; Pred. No. 3.3e-16;
RESULT 1224
ID AAW74465 standard; protein; 205 AA.
DE F11 antigen protein sequence.
PN WO9902561-A1.
PD 21-JAN-1999.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 17.0%; Score 273.5; DB 2; Length 205;
Best Local Similarity 35.1%; Pred. No. 4.6e-14;
RESULT 1225
ID ABG22340 standard; protein; 66 AA.
DE Novel human diagnostic protein #22331.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 16.5%; Score 265; DB 4; Length 66;
Best Local Similarity 98.1%; Pred. No. 5.3e-14;
RESULT 1226
ID ABU69130 standard; protein; 225 AA.
DE Human NOVX polypeptide #5.
PN WO200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Query Match 16.5%; Score 264.5; DB 6; Length 225;
Best Local Similarity 39.0%; Pred. No. 2.8e-13;
RESULT 1227
ID ADO08263 standard; protein; 225 AA.
DE Human NOVX polypeptide #5.
PN US2004018594-A1.
PD 23-JAN-2004.
PA (ALSO) ALSOBROOK J P.
PA (ANDE) ANDERSON D W.
PA (BOLD) BOLDOG F L.
PA (BURG) BURGESS C E.
PA (CASM) CASMAN S J.
PA (CHAP) CHAPOVAL A.
PA (EDIN) EDINGER S R.
PA (GERL) GERLACH V.
PA (GORM) GORMAN L.
PA (GUNT) GUNTHER E.
PA (GUOX) GUO X S.
PA (KEKU) KEKUDA R.
PA (LEPL) LEPLEY D M.
PA (LILL) LI L.
PA (LIUX) LIU X.
PA (MALY) MALYANKAR U M.
PA (MILL) MILLER C E.
PA (PADI) PADIGARU M.
PA (PATT) PATTURAJAN M.
PA (PENA) PENA C E A.
PA (RIEG) RIEGER D K.
PA (SHEN) SHENOY S G.
PA (SHIM) SHIMKETS R A.
PA (SPYT) SPYTEK K A.
PA (TAUP) TAUPIER R J.
PA (VERN) VERNET C A M.
PA (VOSS) VOSS E Z.
PA (ZERH) ZERHUSEN B D.
Query Match 16.5%; Score 264.5; DB 8; Length 225;
Best Local Similarity 39.0%; Pred. No. 2.8e-13;
RESULT 1228
ID AAY08073 standard; protein; 268 AA.
DE Human A33 protein.
PN WO914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 14.8%; Score 238; DB 2; Length 268;
Best Local Similarity 29.0%; Pred. No. 5.3e-11;
RESULT 1229
ID ADH62551 standard; protein; 268 AA.
DE Human A33 antigenic protein fragment #1.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK) ASHKENAZI A.
PA (FONG) FONG S.
PA (GODD) GODDARD A.
PA (GURN) GURNEY A L.
PA (NAPI) NAPIER M A.
PA (TUMA) TUMAS D.
PA (WOOD) WOOD W I.
Query Match 14.8%; Score 238; DB 7; Length 268;
Best Local Similarity 29.0%; Pred. No. 5.3e-11;
RESULT 1230
ID AEL49673 standard; protein; 268 AA.
DE Human A33 antigen precursor, residues 24-183, SEQ ID NO: 24.
PN US2006233803-A1.
PD 19-OCT-2006.
PA (GETH) GENENTECH INC.
Query Match 14.8%; Score 238; DB 10; Length 268;

Best Local Similarity 29.0%; Pred. No. 5.3e-11;
RESULT 1231
ID AAY23327 standard; protein; 270 AA.
DE An A33 related antigen sequence.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match 14.8%; Score 238; DB 2; Length 270;
Best Local Similarity 29.0%; Pred. No. 5.3e-11;
RESULT 1232
ID AAY23329 standard; protein; 273 AA.
DE An A33 related antigen sequence.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match 14.8%; Score 238; DB 2; Length 273;
Best Local Similarity 29.0%; Pred. No. 5.4e-11;
RESULT 1233
ID AAY08075 standard; protein; 273 AA.
DE Human A33 protein fragment #2.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 14.8%; Score 238; DB 2; Length 273;
Best Local Similarity 29.0%; Pred. No. 5.4e-11;
RESULT 1234
ID ADH62533 standard; protein; 273 AA.
DE Human A33 antigenic protein fragment #2.
PN WO2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 14.8%; Score 238; DB 7; Length 273;
Best Local Similarity 29.0%; Pred. No. 5.4e-11;
RESULT 1235
ID AEL49675 standard; protein; 273 AA.
DE Human A33 antigen precursor, residues 12-284, SEQ ID NO: 26.
PN US2006233803-A1.
PD 19-OCT-2006.
PA (GETH) GENENTECH INC.
Query Match 14.8%; Score 238; DB 10; Length 273;
Best Local Similarity 29.0%; Pred. No. 5.4e-11;
RESULT 1236
ID AAN14146 standard; protein; 319 AA.
DE Human A33 antigen.
PN WO9708189-A1.
PD 06-MAR-1997.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 14.8%; Score 238; DB 2; Length 319;
Best Local Similarity 29.0%; Pred. No. 6.6e-11;
RESULT 1237
ID AAY23323 standard; protein; 319 AA.
DE Amino acid sequence of the A33 antigen.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match 14.8%; Score 238; DB 2; Length 319;
Best Local Similarity 29.0%; Pred. No. 6.6e-11;
RESULT 1238
ID AAB65863 standard; protein; 319 AA.
DE Human A33 protein SEQ ID NO: 67.
PN WO200078808-A1.
PD 28-DEC-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 14.8%; Score 238; DB 4; Length 319;
Best Local Similarity 29.0%; Pred. No. 6.6e-11;
RESULT 1239
ID ADA10947 standard; protein; 319 AA.
DE Human A33 molecule.
DE Human cDNA differentially expressed in colon cancer #43 product.
PN US2002160382-A1.
PD 31-OCT-2002.
PA (LASE/) LASEK A W.
PA (JONE/) JONES D A.
Query Match 14.8%; Score 238; DB 6; Length 319;
Best Local Similarity 29.0%; Pred. No. 6.6e-11;
RESULT 1240
ID ADH62533 standard; protein; 319 AA.
DE Human A33 antigenic protein.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 14.8%; Score 238; DB 7; Length 319;
Best Local Similarity 29.0%; Pred. No. 6.6e-11;
RESULT 1241
ID ADN39847 standard; protein; 319 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO: C217.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 14.8%; Score 238; DB 7; Length 319;
Best Local Similarity 29.0%; Pred. No. 6.6e-11;
RESULT 1242
ID ADN35289 standard; protein; 319 AA.
DE Human A33 antigen protein.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 14.8%; Score 238; DB 8; Length 319;
Best Local Similarity 29.0%; Pred. No. 6.6e-11;
RESULT 1243
ID ADP54587 standard; protein; 319 AA.
DE Human PRO protein sequence SEQ ID NO: 563.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 14.8%; Score 238; DB 8; Length 319;
Best Local Similarity 29.0%; Pred. No. 6.6e-11;
RESULT 1244
ID AEB85134 standard; protein; 319 AA.
DE Human novel secreted protein hua33.
PN WO2005058028-A2.
PD 30-JUN-2005.
PA (GETH) GENENTECH INC.
Query Match 14.8%; Score 238; DB 10; Length 319;
Best Local Similarity 29.0%; Pred. No. 6.6e-11;
RESULT 1245
ID AEL49655 standard; protein; 319 AA.
DE Human A33 antigen, SEQ ID NO: 6.
PN US2006233803-A1.
PD 19-OCT-2006.
PA (GETH) GENENTECH INC.
Query Match 14.8%; Score 238; DB 9; Length 319;
Best Local Similarity 29.0%; Pred. No. 6.6e-11;
RESULT 1246
ID ABP62881 standard; protein; 336 AA.
DE Human polypeptide SEQ ID NO 318.
PN WO200218424-A2.
PD 07-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 14.8%; Score 238; DB 5; Length 336;
Best Local Similarity 29.0%; Pred. No. 7.1e-11;
RESULT 1247
ID ADK40854 standard; protein; 316 AA.
DE Human A33 molecule.

PN US6699688-B1.
PD 02-MAR-2004.
PA (UYNV) UNIV NEW YORK STATE RES FOUND.
Query Match 14.6%; Score 234.5; DB 8; Length 316;
Best Local Similarity 28.9%; Pred. No. 1.3e-10;
RESULT 1248
ID ADU66694 standard; protein; 316 AA.
DE Human A33 protein.
PN US2004235768-A1.
PD 25-NOV-2004.
PA (KORN/) KORNECKI E.
PA (SOBO/) SOBOCKA M B.
Query Match 14.6%; Score 234.5; DB 8; Length 316;
Best Local Similarity 28.9%; Pred. No. 1.3e-10;
RESULT 1249
ID ADK40845 standard; protein; 193 AA.
DE Human platelet F11 receptor #2.
PN US6699688-B1.
PD 02-MAR-2004.
PA (UYNV) UNIV NEW YORK STATE RES FOUND.
Query Match 14.0%; Score 224.5; DB 8; Length 193;
Best Local Similarity 34.9%; Pred. No. 4.4e-10;
RESULT 1250
ID ADU6685 standard; protein; 193 AA.
DE Human platelet F11 receptor protein, F11R-B.
PN US2004235768-A1.
PD 25-NOV-2004.
PA (KORN/) KORNECKI E.
PA (SOBO/) SOBOCKA M B.
Query Match 14.0%; Score 224.5; DB 8; Length 193;
Best Local Similarity 34.9%; Pred. No. 4.4e-10;
RESULT 1251
ID ADW97861 standard; protein; 88 AA.
DE Human JAM-1 protein active fragment.
PN US2005025776-A1.
PD 03-FEB-2005.
PA (WEBE/) WEBER C.
Query Match 13.8%; Score 221; DB 9; Length 88;
Best Local Similarity 49.4%; Pred. No. 3.1e-10;
RESULT 1252
ID AAW14158 standard; protein; 318 AA.
DE Mouse A33 antigen.
PN WO9708189-A1.
PD 06-MAR-1997.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 13.6%; Score 219; DB 2; Length 318;
Best Local Similarity 26.9%; Pred. No. 2.4e-09;
RESULT 1253
ID ADC78359 standard; protein; 389 AA.
DE Human PRO246 protein.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 13.3%; Score 213.5; DB 3; Length 389;
Best Local Similarity 29.1%; Pred. No. 8.7e-09;
RESULT 1254
ID ADO43535 standard; protein; 348 AA.
DE Amino acid sequence of an additional human A34 clone.
PN WO2004037999-A2.
PD 06-MAY-2004.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 13.2%; Score 211.5; DB 8; Length 348;
Best Local Similarity 25.8%; Pred. No. 1.1e-08;
RESULT 1255
ID ADP55948 standard; protein; 370 AA.
DE Human PRO protein sequence SEQ ID NO:1924.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 13.2%; Score 211.5; DB 8; Length 370;
Best Local Similarity 25.8%; Pred. No. 1.2e-08;
RESULT 1256
ID AAY08621 standard; protein; 387 AA.
DE Human secreted protein AJ26_3.
PN WO9926972-A1.
PD 03-JUN-1999.
PA (GEMY) GENETICS INST INC.
Query Match 13.2%; Score 211.5; DB 2; Length 387;
Best Local Similarity 25.8%; Pred. No. 1.3e-08;
RESULT 1257
ID AAY67312 standard; protein; 387 AA.
DE Human secreted protein AJ26_3 amino acid sequence.
PN WO9960020-A1.
PD 25-NOV-1999.
PA (GEMY) GENETICS INST INC.
Query Match 13.2%; Score 211.5; DB 3; Length 387;
Best Local Similarity 25.8%; Pred. No. 1.3e-08;
RESULT 1258
ID ADC38775 standard; protein; 387 AA.
DE Human secreted protein #62.
PN US2002193567-A1.
PD 19-DEC-2002.
PA (GEMY) GENETICS INST INC.
Query Match 13.2%; Score 211.5; DB 7; Length 387;
Best Local Similarity 25.8%; Pred. No. 1.3e-08;
RESULT 1259
ID ADO43531 standard; protein; 387 AA.
DE Amino acid sequence of a full length human A34 protein.
PN WO2004037999-A2.
PD 06-MAY-2004.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 13.2%; Score 211.5; DB 8; Length 387;
Best Local Similarity 25.8%; Pred. No. 1.3e-08;
RESULT 1260
ID ADO43533 standard; protein; 402 AA.
DE Amino acid sequence of a human A34 protein.
PN WO2004037999-A2.
PD 06-MAY-2004.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 13.2%; Score 211.5; DB 8; Length 402;
Best Local Similarity 25.8%; Pred. No. 1.3e-08;
RESULT 1261
ID AAY76303 standard; protein; 389 AA.
DE Fragment of human secreted protein encoded by gene 29.
PN WO9958660-A1.
PD 18-NOV-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.1%; Score 211; DB 3; Length 389;
Best Local Similarity 27.9%; Pred. No. 1.4e-08;
RESULT 1262
ID ADE11956 standard; protein; 389 AA.
DE Human secreted polypeptide #210.
PN US2003100051-A1.
PD 29-MAY-2003.
PA (RUBE/) RUBEN S M.
PA (NIJU/) FLORENCE K A.
PA (NIJU/) NI J.
PA (ROSE/) ROSEN C A.
PA (CART/) CARTER K C.
PA (MOOR/) MOORE P A.
PA (OLSE/) OLSEN H S.
PA (SHIY/) SHI Y.
PA (YOUN/) YOUNG P E.
PA (WEIY/) WEI Y.
PA (BREW/) BREWER L A.
PA (SOPP/) SOPP D R.
PA (LAFI/) LAFLEUR D W.
PA (ENDR/) ENDRESS G A.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
Query Match 13.1%; Score 211; DB 7; Length 389;
Best Local Similarity 27.9%; Pred. No. 1.4e-08;
RESULT 1263
ID ADC42841 standard; protein; 423 AA.
DE REMAP protein #1.
PN WO2003027228-A2.

PD 03-APR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 13.1%; Score 211; DB 7; Length 423;
Best Local Similarity 24.5%; Pred. No. 1.6e-08;
RESULT 1264
ID AAB90818 standard; protein; 390 AA.
DE Human shear stress-response protein SEQ ID NO: 144.
PN WO200125427-A1.
PD 12-APR-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
PA (NOJI) NOJIMA H.
Query Match 13.1%; Score 210.5; DB 4; Length 390;
Best Local Similarity 26.3%; Pred. No. 1.5e-08;
RESULT 1265
ID AAV05286 standard; protein; 390 AA.
DE EGF-like homologue PRO246.
PN WO9914327-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 2; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1266
ID AAV13351 standard; protein; 390 AA.
DE Amino acid sequence of protein PRO246.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 2; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1267
ID AAV27096 standard; protein; 390 AA.
DE Human viral receptor protein (ACVRP).
PN US942606-A.
PD 24-AUG-1999.
PA (INCY-) INCYTE PHARM INC.
Query Match 13.1%; Score 210; DB 2; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1268
ID AAY94999 standard; protein; 390 AA.
DE Human secreted protein vc51_1, SEQ ID NO:38.
PN WO200011015-A1.
PD 02-MAR-2000.
PA (ALPH-) ALPHAGENE INC.
Query Match 13.1%; Score 210; DB 3; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1269
ID AAY88574 standard; protein; 390 AA.
DE Human PRO246 amino acid sequence.
PN WO200015666-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 3; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1270
ID AAB80219 standard; protein; 390 AA.
DE Human PRO246 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 4; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1271
ID AAE06610 standard; protein; 390 AA.
DE Human protein having hydrophobic domain, HP10801.
PN WO200149728-A2.
PD 12-JUL-2001.
PA (PROT-) PROTEGENE INC.
PA (SAGA) SAGAMI CHEM RES CENT.
Query Match 13.1%; Score 210; DB 4; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1272
ID AAB31207 standard; protein; 390 AA.
DE Amino acid sequence of human polypeptide PRO246.
PN WO2000077037-A2.
PD 21-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 4; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1273
ID AAU12340 standard; protein; 390 AA.
DE Human PRO246 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 4; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1274
ID AAB53082 standard; protein; 390 AA.
DE Human angiogenesis-associated protein PRO246, SEQ ID NO:96.
PN WO200053753-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 4; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1275
ID AAB68599 standard; protein; 390 AA.
DE PRO246.
PN WO200105836-A1.
PD 25-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 4; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1276
ID AAB88358 standard; protein; 390 AA.
DE Human membrane or secretory protein clone PSEC0086.
PN EP1067182-A2.
PD 10-JAN-2001.
PA (HELI-) HELIX RES INST.
Query Match 13.1%; Score 210; DB 4; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1277
ID ABU71597 standard; protein; 390 AA.
DE Human PRO polypeptide #8.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1278
ID ABO17784 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1279
ID ABU71452 standard; protein; 390 AA.
DE Human PRO polypeptide #8.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1280
ID ADA56949 standard; protein; 390 AA.
DE Human secreted protein #232.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1281
ID ABO25178 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003040014-A1.

PD 27-FEB-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1291
ID ABUS9819 standard; protein; 390 AA.
DE Novel secreted and transmembrane protein PRO246.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1292
ID ABO25009 standard; protein; 390 AA.
DE Human secreted/transmembrane protein (PRO) #169.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1293
ID ABU64506 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1294
ID ABU72064 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2002177165-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1295
ID ABU67352 standard; protein; 390 AA.
DE Human secreted protein PRO246.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1296
ID ABU67165 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003032062-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1297
ID ABO14872 standard; protein; 390 AA.
DE Human secreted / transmembrane polypeptide PRO246.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1298
ID ABU67014 standard; protein; 390 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 338.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1299
ID ABU69629 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.

PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1282
ID ABU81038 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1283
ID ABU71898 standard; protein; 390 AA.
DE Human secreted/transmembrane protein PRO246.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1284
ID ABO01781 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1285
ID ABU66738 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1286
ID ABU54354 standard; protein; 390 AA.
DE Human secreted/transmembrane protein PRO246.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1287
ID ADA40800 standard; protein; 390 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1288
ID ABU67296 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003032063-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1289
ID ABO47369 standard; protein; 390 AA.
DE Human secreted/transmembrane polypeptide PRO246.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1290
ID ABR47754 standard; protein; 390 AA.
DE Human secreted protein, SEQ ID 645.
PN WO200295010-A2.
PD 28-NOV-2002.

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Query Match
Best Local Similarity 13.1%; Score 210; DB 6; Length 390;
RESULT 1300
ID ADU79807 standard; protein; 390 AA.
DE Human secreted/transmembrane protein PRO246.
PN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 6; Length 390;
RESULT 1301
ID ABO14811 standard; protein; 390 AA.
DE Human secreted / transmembrane polypeptide PRO246.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 6; Length 390;
RESULT 1302
ID ADA45857 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 6; Length 390;
RESULT 1303
ID ADA76288 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 6; Length 390;
RESULT 1304
ID ADB29244 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 6; Length 390;
RESULT 1305
ID ADA18938 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 6; Length 390;
RESULT 1306
ID ADA61561 standard; protein; 390 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 6; Length 390;
RESULT 1307
ID ADB19346 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 6; Length 390;
RESULT 1308
ID ADB27887 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 6; Length 390;
RESULT 1309
ID ADA86366 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 6; Length 390;
RESULT 1310
ID ADB15930 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 6; Length 390;
RESULT 1311
ID ADA47716 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 6; Length 390;
RESULT 1312
ID ADA18100 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 6; Length 390;
RESULT 1313
ID ABO32763 standard; protein; 390 AA.
DE Human secreted/transmembrane protein PRO246.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 6; Length 390;
RESULT 1314
ID ADA67511 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003088795-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 6; Length 390;
RESULT 1315
ID ADB30518 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 6; Length 390;
RESULT 1316
ID ADA85814 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 6; Length 390;
RESULT 1317
ID ADA97026 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 6; Length 390;
RESULT 1318
ID ADB27887 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 6; Length 390;
RESULT 1319
ID ADA86366 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
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RESULT 1318
ID ADA79330 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1319
ID ADA87469 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1320
ID ADB16671 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1321
ID ABO34823 standard; protein; 390 AA.
DE Human PRO polypeptide #8.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1322
ID ADA16075 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1323
ID ADA91763 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1324
ID ADB14826 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1325
ID ADA47282 standard; protein; 390 AA.
DE Human secreted/transmembrane polypeptide PRO246.
PN US2003044844-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1326
ID ADB18787 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1327
ID ADA85262 standard; protein; 390 AA.

ID ADA94002 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1328
ID ADB19898 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1329
ID ADB13210 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1330
ID ABO43317 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1331
ID ADA74464 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1332
ID ADA42220 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1333
ID ADB24697 standard; protein; 390 AA.
DE Human PRO polypeptide SEQ ID NO 338.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1334
ID ADA82221 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1335
ID ADA75184 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1336
ID ADA85262 standard; protein; 390 AA.

DE Novel human secreted and transmembrane protein PRO246.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1337
ID ADA84710 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1338
ID ABO53064 standard; protein; 390 AA.
DE Human putative spliceosome associated protein (SAP) #41.
PN US2003068803-A1.
PD 10-APR-2003.
PA (REED/) REED R.
PA (ZHOU/) ZHOU Z.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1339
ID ABO17501 standard; protein; 390 AA.
DE Human PRO polypeptide #8.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1340
ID ADB29966 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1341
ID ADA80494 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1342
ID ADA75736 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1343
ID ADA46961 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1344
ID ADB25257 standard; protein; 390 AA.
DE Human PRO polypeptide SEQ ID NO 338.
PN US200307715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1345
ID ADA93433 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US200307721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1346
ID ADB26783 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1347
ID ADB31070 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1348
ID ADA60998 standard; protein; 390 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1349
ID ADB24145 standard; protein; 390 AA.
DE Human PRO polypeptide SEQ ID NO 338.
PN US200307714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1350
ID ADA96474 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1351
ID ADA81046 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1352
ID ADA95922 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1353
ID ADB26231 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1354
ID ADB21716 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.

PN US2003082765-A1.
 PA (GETH) GENENTECH INC.
 Query Match 13.1%; Score 210; DB 6; Length 390;
 Best Local Similarity 27.9%; Pred. No. 1.7e-08;
 RESULT 1355
 ID ADA77495 standard; protein; 390 AA.
 DE Human PRO polypeptide #169.
 PN US2003068797-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 13.1%; Score 210; DB 7; Length 390;
 Best Local Similarity 27.9%; Pred. No. 1.7e-08;
 RESULT 1356
 ID ADB18235 standard; protein; 390 AA.
 DE Human PRO polypeptide #169.
 PN US2003077710-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 13.1%; Score 210; DB 7; Length 390;
 Best Local Similarity 27.9%; Pred. No. 1.7e-08;
 RESULT 1357
 ID ADA86918 standard; protein; 390 AA.
 DE Novel human secreted and transmembrane protein PRO246.
 PN US2003082709-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 13.1%; Score 210; DB 7; Length 390;
 Best Local Similarity 27.9%; Pred. No. 1.7e-08;
 RESULT 1358
 ID ADA16499 standard; protein; 390 AA.
 DE Human secreted/transmembrane protein, #9.
 PN US2003039969-A1.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 13.1%; Score 210; DB 7; Length 390;
 Best Local Similarity 27.9%; Pred. No. 1.7e-08;
 RESULT 1359
 ID ADA12928 standard; protein; 390 AA.
 DE Human secreted/transmembrane protein, #9.
 PN US2003049622-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 13.1%; Score 210; DB 7; Length 390;
 Best Local Similarity 27.9%; Pred. No. 1.7e-08;
 RESULT 1360
 ID ADA41796 standard; protein; 390 AA.
 DE Human secreted/transmembrane protein, #9.
 PN US2003082540-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 13.1%; Score 210; DB 7; Length 390;
 Best Local Similarity 27.9%; Pred. No. 1.7e-08;
 RESULT 1361
 ID ADA88021 standard; protein; 390 AA.
 DE Novel human secreted and transmembrane protein PRO246.
 PN US2003082700-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 13.1%; Score 210; DB 7; Length 390;
 Best Local Similarity 27.9%; Pred. No. 1.7e-08;
 RESULT 1362
 ID ADA46409 standard; protein; 390 AA.
 DE Novel human secreted and transmembrane protein PRO246.
 PN US2003054516-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 13.1%; Score 210; DB 7; Length 390;
 Best Local Similarity 27.9%; Pred. No. 1.7e-08;
 RESULT 1363
 ID ADA17143 standard; protein; 390 AA.
 DE Human secreted/transmembrane protein, #9.
 PN US2003017498-A1.

PD 23-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 13.1%; Score 210; DB 7; Length 390;
 Best Local Similarity 27.9%; Pred. No. 1.7e-08;
 RESULT 1364
 ID ADA42646 standard; protein; 390 AA.
 DE Human secreted/transmembrane protein, #9.
 PN US2003054351-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 13.1%; Score 210; DB 7; Length 390;
 Best Local Similarity 27.9%; Pred. No. 1.7e-08;
 RESULT 1365
 ID ADB28439 standard; protein; 390 AA.
 DE Human PRO polypeptide #169.
 PN US2003082699-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 13.1%; Score 210; DB 7; Length 390;
 Best Local Similarity 27.9%; Pred. No. 1.7e-08;
 RESULT 1366
 ID ADB28991 standard; protein; 390 AA.
 DE Human PRO polypeptide #169.
 PN US2003082706-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 13.1%; Score 210; DB 7; Length 390;
 Best Local Similarity 27.9%; Pred. No. 1.7e-08;
 RESULT 1367
 ID ADA76943 standard; protein; 390 AA.
 DE Human PRO polypeptide #169.
 PN US2003059909-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 13.1%; Score 210; DB 7; Length 390;
 Best Local Similarity 27.9%; Pred. No. 1.7e-08;
 RESULT 1368
 ID ADA88573 standard; protein; 390 AA.
 DE Novel human secreted and transmembrane protein PRO246.
 PN US2003073213-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 13.1%; Score 210; DB 7; Length 390;
 Best Local Similarity 27.9%; Pred. No. 1.7e-08;
 RESULT 1369
 ID ADA97578 standard; protein; 390 AA.
 DE Human PRO polypeptide #169.
 PN US2003082686-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 13.1%; Score 210; DB 7; Length 390;
 Best Local Similarity 27.9%; Pred. No. 1.7e-08;
 RESULT 1370
 ID ADB27335 standard; protein; 390 AA.
 DE Human PRO polypeptide #169.
 PN US2003022239-A1.
 PD 30-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 13.1%; Score 210; DB 7; Length 390;
 Best Local Similarity 27.9%; Pred. No. 1.7e-08;
 RESULT 1371
 ID ADB22268 standard; protein; 390 AA.
 DE Novel human secreted and transmembrane protein PRO246.
 PN US2003087344-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 13.1%; Score 210; DB 7; Length 390;
 Best Local Similarity 27.9%; Pred. No. 1.7e-08;
 RESULT 1372
 ID ABO19865 standard; protein; 390 AA.
 DE Human secreted/transmembrane protein PRO246.
 PN US2003044902-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 13.1%; Score 210; DB 7; Length 390;

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Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1373
ID ABO17562 standard; protein; 390 AA.
DE Human PRO polypeptide #8.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1374
ID ADA66959 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US200308793-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1375
ID ADB22820 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US200307711-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1376
ID ADB23593 standard; protein; 390 AA.
DE Human PRO polypeptide SEQ ID NO 338.
PN US200307712-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1377
ID ADA92315 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1378
ID ADB15378 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1379
ID ADB38630 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1380
ID ADB38078 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1381
ID ADB66550 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1382
ID ADB89630 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1383
ID ADB90362 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1384
ID ADB77565 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1385
ID ADB39463 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1386
ID ADB74701 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1387
ID ADB47086 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1388
ID ADB86693 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1389
ID ADB77298 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1390
ID ADB34455 standard; protein; 390 AA.
DE Human PRO polypeptide SEQ ID NO 338.
PN US200307717-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1391
ID ADB34455 standard; protein; 390 AA.
DE Human PRO polypeptide SEQ ID NO 338.
PN US200307717-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
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ID ADB35559 standard; protein; 390 AA.
DE Human PRO polypeptide SEQ ID NO 338.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1392
ID ADB33903 standard; protein; 390 AA.
DE Human PRO polypeptide SEQ ID NO 338.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1393
ID ADB35007 standard; protein; 390 AA.
DE Human PRO polypeptide SEQ ID NO 338.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1394
ID ADB36111 standard; protein; 390 AA.
DE Human PRO polypeptide SEQ ID NO 338.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1395
ID ADB46506 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1396
ID ADC28347 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1397
ID ADC39547 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1398
ID ADC40061 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1399
ID ADC18889 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1400
ID ADC34185 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1401
ID ADC29240 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1402
ID ADC28771 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1403
ID ADC40656 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1404
ID ADC19313 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1405
ID ADC33761 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1406
ID ADC12831 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1407
ID ADC50379 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1408
ID ADC71926 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1409
ID ADC59905 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.

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PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 7; Length 390;
RESULT 1410
ID ADC52912 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein Seq ID338.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 7; Length 390;
RESULT 1411
ID ADC57266 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein Seq ID338.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 7; Length 390;
RESULT 1412
ID ADC60457 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 7; Length 390;
RESULT 1413
ID ADC50932 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 7; Length 390;
RESULT 1414
ID ADC65459 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 7; Length 390;
RESULT 1415
ID ADC54557 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein Seq ID338.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 7; Length 390;
RESULT 1416
ID ADC53518 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein Seq ID338.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 7; Length 390;
RESULT 1417
ID ADC59041 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein Seq ID338.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 7; Length 390;
RESULT 1418
ID ADC55919 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein Seq ID338.
PN US2003087360-A1.

PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 7; Length 390;
RESULT 1419
ID ADC58489 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein Seq ID338.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 7; Length 390;
RESULT 1420
ID ADC12283 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 7; Length 390;
RESULT 1421
ID ADD03163 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 7; Length 390;
RESULT 1422
ID ADC90155 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 7; Length 390;
RESULT 1423
ID ADC69574 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 7; Length 390;
RESULT 1424
ID ADC48463 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 7; Length 390;
RESULT 1425
ID ADD09992 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 7; Length 390;
RESULT 1426
ID ADD04567 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.1%; Score 210; DB 7; Length 390;
RESULT 1427
ID ADC80523 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003092103-A1.
PD 15-MAY-2003.
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PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1428
ID ADD11030 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1429
ID ADC47911 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1430
ID ADD04838 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1431
ID ADC79971 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1432
ID ADD09440 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1433
ID ADD03844 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1434
ID ADD03420 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1435
ID ADD41153 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1436
ID ADD52292 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1437
ID ADD53032 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1438
ID ADD53584 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1439
ID ADD51740 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1440
ID ADD02539 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1441
ID ADD01973 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1442
ID ADD54155 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1443
ID ADD92472 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1444
ID ADD91368 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1445
ID ADE03982 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;

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.Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1446
ID ADE32279 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1447
ID ADE22211 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1448
ID ADD79435 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1449
ID ADE41971 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1450
ID ADE17788 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1451
ID ADD91920 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1452
ID ADE33383 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1453
ID ADE33935 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1454
ID ADD79987 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1455
ID ADD93024 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1456
ID ADE19444 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1457
ID ADE34672 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1458
ID ADE18892 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1459
ID ADE43088 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1460
ID ADD95877 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1461
ID ADE22763 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1462
ID ADD78881 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1463
ID ADE32831 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1464
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ID ADE42523 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1465
ID ADD80539 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1466
ID ADD89567 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1467
ID ADE40851 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1468
ID ADE04650 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1469
ID ADE92779 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1470
ID ADG21488 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1471
ID ADG23129 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1472
ID ADF97464 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1473
ID ADG80528 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1474
ID ADG79976 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1475
ID ADG63791 standard; protein; 390 AA.
DE Human secreted/transmembrane polypeptide PRO246.
PN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1476
ID ADH59155 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1477
ID ADH55268 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1478
ID ADH55820 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1479
ID ADI37934 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1480
ID ADI64039 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1481
ID ADI64988 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1482
ID ADI63487 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.

PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1483
ID ADH81901 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1484
ID ADH81349 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1485
ID ADJ26202 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1486
ID ADM82518 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1487
ID ADN15917 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1488
ID ADN16546 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1489
ID ADN15365 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1490
ID ADN14813 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003067357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1491
ID ADC81075 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003092115-A1.

PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1492
ID ADE79117 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1493
ID ADD76523 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1494
ID ADD87887 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1495
ID ADD86291 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1496
ID ADE79541 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1497
ID ADE75739 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1498
ID ADE73217 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1499
ID ADE23315 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
RESULT 1500
ID ADE23867 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003092110-A1.
PD 15-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.7e-08;
5..

GenCore version 6.2
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OM protein - protein search, using sw model

Run on: April 10, 2007, 16:31:05 ; Search time 52 Seconds
(without alignments)
525.184 Million cell updates/sec

Title: US-10-785-221a-9

Perfect score: 1605

Sequence: 1 MARRGRHRLLLRLRYVVA.....TPVIPALWKAAGSRGQEF 312

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Issued Patents AA:*

1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5 COMB.pep.*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6 COMB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7 COMB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H COMB.pep.*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS COMB.pep.*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE COMB.pep.*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1605	100.0	312	2	US-09-254-465A-9
2	1605	100.0	312	2	US-09-907-794A-64
3	1605	100.0	312	2	US-09-905-125A-64
4	1605	100.0	312	2	US-09-902-775A-64
5	1605	100.0	312	2	US-09-906-700-64
6	1605	100.0	312	2	US-09-903-603A-64
7	1605	100.0	312	2	US-09-904-920A-64
8	1605	100.0	312	2	US-09-909-064-64
9	1605	100.0	312	2	US-09-905-381A-64
10	1605	100.0	312	2	US-09-906-618-64
11	1605	100.0	312	2	US-09-953-499-9
12	1605	100.0	312	2	US-09-906-646-64
13	1605	100.0	312	2	US-09-904-462-64
14	1605	100.0	312	2	US-09-902-736A-64
15	1605	100.0	312	2	US-09-906-722A-64
16	1605	100.0	312	2	US-09-905-449-64
17	1605	100.0	312	2	US-09-903-562B-64
18	1605	100.0	312	2	US-09-906-679A-64
19	1605	100.0	312	3	US-09-907-841-64
20	1465	91.3	298	2	US-09-152-060-76
21	1465	91.3	298	2	US-09-852-797-76
22	1465	91.3	298	2	US-09-853-161-76
23	1465	91.3	298	2	US-10-058-993-76
24	461.5	28.8	310	2	US-09-907-794A-423
25	461.5	28.8	310	2	US-09-905-125A-423
26	461.5	28.8	310	2	US-09-902-775A-423

27	461.5	28.8	310	2	US-09-906-700-423	Sequence 423, App
28	461.5	28.8	310	2	US-09-903-603A-423	Sequence 423, App
29	461.5	28.8	310	2	US-09-904-920A-423	Sequence 423, App
30	461.5	28.8	310	2	US-09-909-064-423	Sequence 423, App
31	461.5	28.8	310	2	US-09-905-381A-423	Sequence 423, App
32	461.5	28.8	310	2	US-09-906-618-423	Sequence 423, App
33	461.5	28.8	310	2	US-09-906-646-423	Sequence 423, App
34	461.5	28.8	310	2	US-09-904-462-423	Sequence 423, App
35	461.5	28.8	310	2	US-09-902-736A-423	Sequence 423, App
36	461.5	28.8	310	2	US-10-033-301-20	Sequence 20, Appl
37	461.5	28.8	310	2	US-09-906-722A-423	Sequence 423, App
38	461.5	28.8	310	2	US-09-905-449-423	Sequence 423, App
39	461.5	28.8	310	2	US-09-903-562B-423	Sequence 423, App
40	461.5	28.8	310	2	US-10-033-435-20	Sequence 20, Appl
41	461.5	28.8	310	2	US-09-906-679A-423	Sequence 423, App
42	461.5	28.8	310	3	US-09-907-841-423	Sequence 423, App
43	405	25.2	299	2	US-09-188-930-189	Sequence 189, App
44	404	25.2	299	2	US-09-188-930-331	Sequence 331, App
45	404	25.2	299	2	US-09-462-270-2	Sequence 2, Appl
46	404	25.2	299	2	US-09-254-465A-1	Sequence 189, App
47	404	25.2	299	2	US-09-312-283C-119	Sequence 312, App
48	404	25.2	299	2	US-09-312-283C-331	Sequence 331, App
49	404	25.2	299	2	US-09-907-794A-119	Sequence 119, App
50	404	25.2	299	2	US-09-905-125A-119	Sequence 119, App
51	404	25.2	299	2	US-09-902-775A-119	Sequence 119, App
52	404	25.2	299	2	US-09-397-243D-3	Sequence 3, Appl
53	404	25.2	299	2	US-09-906-700-119	Sequence 119, App
54	404	25.2	299	2	US-09-903-603A-119	Sequence 119, App
55	404	25.2	299	2	US-09-904-920A-119	Sequence 119, App
56	404	25.2	299	2	US-09-909-064-119	Sequence 119, App
57	404	25.2	299	2	US-09-905-381A-119	Sequence 119, App
58	404	25.2	299	2	US-09-906-618-119	Sequence 119, App
59	404	25.2	299	2	US-09-953-499-1	Sequence 1, Appl
60	404	25.2	299	2	US-09-906-646-119	Sequence 119, App
61	404	25.2	299	2	US-09-904-462-119	Sequence 119, App
62	404	25.2	299	2	US-09-902-736A-119	Sequence 119, App
63	404	25.2	299	2	US-09-906-722A-119	Sequence 119, App
64	404	25.2	299	2	US-09-905-449-119	Sequence 119, App
65	404	25.2	299	2	US-09-903-562B-119	Sequence 119, App
66	404	25.2	299	2	US-09-906-679A-119	Sequence 119, App
67	404	25.2	299	3	US-09-907-841-119	Sequence 119, App
68	401	25.0	260	2	US-09-254-465A-23	Sequence 23, Appl
69	401	25.0	260	2	US-09-953-499-23	Sequence 23, Appl
70	401	25.0	263	2	US-09-254-465A-25	Sequence 25, Appl
71	401	25.0	263	2	US-09-953-499-25	Sequence 25, Appl
72	394	24.5	300	2	US-09-254-465A-10	Sequence 10, Appl
73	394	24.5	300	2	US-09-397-243D-12	Sequence 12, Appl
74	394	24.5	300	2	US-09-953-499-10	Sequence 10, Appl
75	273.5	17.0	205	2	US-09-462-270-4	Sequence 4, Appl
76	238	14.8	270	2	US-09-254-465A-24	Sequence 24, Appl
77	238	14.8	270	2	US-09-953-499-24	Sequence 24, Appl
78	238	14.8	273	2	US-09-254-465A-26	Sequence 26, Appl
79	238	14.8	273	2	US-09-953-499-26	Sequence 26, Appl
80	238	14.8	319	1	US-08-597-495B-22	Sequence 22, Appl
81	238	14.8	319	2	US-09-068-051A-22	Sequence 22, Appl
82	238	14.8	319	2	US-09-336-536-57	Sequence 67, Appl
83	238	14.8	319	2	US-09-254-465A-6	Sequence 6, Appl
84	238	14.8	319	2	US-09-953-499-6	Sequence 6, Appl
85	234.5	14.6	316	2	US-09-397-243D-13	Sequence 13, Appl
86	224.5	14.0	193	2	US-09-397-243D-4	Sequence 4, Appl
87	222	13.8	318	2	US-09-068-051A-32	Sequence 32, Appl
88	211.5	13.2	387	2	US-09-175-528-2	Sequence 2, Appl
89	210	13.1	390	1	US-08-979-424-1	Sequence 1, Appl
90	210	13.1	390	2	US-09-907-794A-39	Sequence 39, Appl
91	210	13.1	390	2	US-09-905-125A-39	Sequence 39, Appl
92	210	13.1	390	2	US-09-902-775A-39	Sequence 39, Appl
93	210	13.1	390	2	US-09-906-700-39	Sequence 39, Appl
94	210	13.1	390	2	US-09-903-603A-39	Sequence 39, Appl
95	210	13.1	390	2	US-09-904-920A-39	Sequence 39, Appl
96	210	13.1	390	2	US-09-909-064-39	Sequence 39, Appl
97	210	13.1	390	2	US-09-905-381A-39	Sequence 39, Appl
98	210	13.1	390	2	US-09-906-618-39	Sequence 39, Appl
99	210	13.1	390	2	US-09-906-646-39	Sequence 39, Appl

100	210	13.1	390	2	US-09-904-462-39	Sequence 39, Appl	173	162	10.1	1367	1	US-07-977-451-6	Sequence 6, Appl
101	210	13.1	390	2	US-09-902-736A-39	Sequence 39, Appl	174	162	10.1	1367	1	US-07-946-507-4	Sequence 4, Appl
102	210	13.1	390	2	US-09-906-722A-39	Sequence 39, Appl	175	162	10.1	1367	1	US-08-252-517-6	Sequence 6, Appl
103	210	13.1	390	2	US-09-905-449-39	Sequence 39, Appl	176	162	10.1	1367	1	US-07-906-397A-6	Sequence 6, Appl
104	210	13.1	390	2	US-09-903-562B-39	Sequence 39, Appl	177	162	10.1	1367	1	US-08-601-891-6	Sequence 2, Appl
105	210	13.1	390	2	US-09-906-679A-39	Sequence 39, Appl	178	162	10.1	1367	1	US-08-443-861-2	Sequence 2, Appl
106	210	13.1	390	3	US-09-907-841-39	Sequence 39, Appl	179	162	10.1	1367	1	US-09-021-324-6	Sequence 2, Appl
107	207.5	12.9	394	2	US-09-336-536-39	Sequence 39, Appl	180	162	10.1	1367	1	US-08-193-829B-2	Sequence 2, Appl
108	203	12.6	370	2	US-09-336-536-28	Sequence 28, Appl	181	162	10.1	1367	2	US-09-872-136B-6	Sequence 2, Appl
109	202	12.6	76	2	US-09-397-243D-11	Sequence 11, Appl	182	162	10.1	1367	2	US-09-766-678-2	Sequence 2, Appl
110	200	12.5	365	2	US-09-336-536-40	Sequence 40, Appl	183	162	10.1	1367	2	US-09-919-408A-6	Sequence 6, Appl
111	199.5	12.4	341	2	US-09-336-536-29	Sequence 29, Appl	184	162	10.1	1367	5	PCT-US92-02750-8	Sequence 8, Appl
112	199	12.4	383	2	US-09-949-016-11050	Sequence 11050, A	185	162	10.1	1367	5	PCT-US92-05401-6	Sequence 6, Appl
113	198.5	12.4	352	2	US-09-991-181-505	Sequence 505, App	186	162	10.1	1367	5	PCT-US92-09893-6	Sequence 22, Appl
114	198.5	12.4	352	2	US-09-990-444-505	Sequence 505, App	187	161.5	10.1	423	2	US-09-778-510-22	Sequence 22, Appl
115	198.5	12.4	352	2	US-09-997-333-505	Sequence 505, App	188	161	10.0	365	2	US-09-949-016-7591	Sequence 7591, Ap
116	198.5	12.4	352	2	US-09-992-598-505	Sequence 505, App	189	160	10.0	837	2	US-09-949-016-6515	Sequence 6515, Ap
117	198.5	12.4	352	2	US-09-989-735-505	Sequence 505, App	190	159.5	9.9	961	3	US-10-162-335-42	Sequence 42, Appl
118	198.5	12.4	352	3	US-09-989-726-505	Sequence 505, App	191	159	9.9	819	2	US-09-949-016-11044	Sequence 11044, A
119	198.5	12.4	352	3	US-09-997-514-505	Sequence 505, App	192	158	9.8	491	2	US-10-094-749-2150	Sequence 4, Appl
120	198.5	12.4	352	3	US-09-989-728-505	Sequence 505, App	193	157	9.8	330	1	US-08-525-864A-4	Sequence 2, Appl
121	198.5	12.4	352	3	US-09-997-349-505	Sequence 505, App	194	157	9.8	754	1	US-08-525-864A-2	Sequence 1, Appl
122	198.5	12.4	352	3	US-09-997-653-505	Sequence 505, App	195	156.5	9.8	421	1	US-08-659-984A-1	Sequence 1, Appl
123	198.5	12.4	352	3	US-09-989-293A-505	Sequence 505, App	196	156.5	9.8	421	2	US-08-660-531-1	Sequence 1, Appl
124	198.5	12.4	365	1	US-08-978-424-3	Sequence 3, Appl	197	156.5	9.8	421	2	US-09-404-578-1	Sequence 1, Appl
125	198.5	12.4	365	2	US-09-272-496-2	Sequence 2, Appl	198	156.5	9.8	444	1	US-08-659-984A-5	Sequence 5, Appl
126	198.5	12.4	365	2	US-09-949-016-6064	Sequence 6064, Ap	199	156.5	9.8	444	1	US-08-660-531-5	Sequence 5, Appl
127	194.5	12.1	365	2	US-08-928-383B-2	Sequence 2, Appl	200	156.5	9.8	444	2	US-09-404-578-5	Sequence 5, Appl
128	193.5	12.1	317	2	US-10-104-047-3036	Sequence 3036, Ap	201	156	9.7	306	2	US-10-191-029-12	Sequence 12, Appl
129	189	11.8	249	2	US-09-336-536-42	Sequence 42, Appl	202	155.5	9.7	421	2	US-09-569-611C-36	Sequence 36, Appl
130	188	11.7	365	2	US-08-928-383B-23	Sequence 23, Appl	203	155	9.7	298	2	US-09-864-675-4	Sequence 4, Appl
131	188	11.7	365	2	US-08-928-383B-24	Sequence 24, Appl	204	155	9.7	330	2	US-09-864-675-2	Sequence 2, Appl
132	188	11.7	365	2	US-09-899-634C-4	Sequence 4, Appl	205	154.5	9.6	4391	2	US-10-006-011A-2	Sequence 2, Appl
133	185	11.5	365	2	US-08-928-383B-26	Sequence 26, Appl	206	152.5	9.5	398	2	US-09-778-510-4	Sequence 4, Appl
134	183.5	11.4	246	2	US-09-336-536-31	Sequence 31, Appl	207	152	9.5	615	1	US-08-752-307B-9	Sequence 9, Appl
135	181.5	11.3	261	2	US-09-899-634C-2	Sequence 2, Appl	208	152	9.5	615	2	US-09-707-802-9	Sequence 9, Appl
136	178.5	11.1	466	2	US-09-604-107A-8	Sequence 8, Appl	209	152	9.5	615	2	US-09-991-326-9	Sequence 9, Appl
137	171.5	10.7	5512	2	US-09-953-096-2	Sequence 2, Appl	210	151.5	9.4	588	2	US-09-949-016-10547	Sequence 10547, A
138	171	10.7	512	2	US-10-094-749-2493	Sequence 2493, Ap	211	151.5	9.4	733	2	US-10-094-749-3192	Sequence 3192, Ap
139	168.5	10.5	329	2	US-10-104-047-3709	Sequence 3709, Ap	212	151.5	9.4	848	2	US-09-787-443-44	Sequence 44, Appl
140	166.5	10.4	442	2	US-09-778-510-20	Sequence 20, Appl	213	150.5	9.4	296	2	US-09-569-611C-34	Sequence 34, Appl
141	166.5	10.4	442	2	US-09-930-803-1	Sequence 1, Appl	214	150	9.3	198	2	US-09-569-611C-34	Sequence 34, Appl
142	166.5	10.4	4126	2	US-09-953-096-4	Sequence 4, Appl	215	150	9.3	1501	1	US-08-447-464-3	Sequence 3, Appl
143	163.5	10.2	373	2	US-09-991-181-503	Sequence 503, App	216	150	9.3	1501	1	US-08-716-679-3	Sequence 3, Appl
144	163.5	10.2	373	2	US-09-993-833A-59	Sequence 59, App	217	149.5	9.3	349	2	US-09-924-103-4	Sequence 4, Appl
145	163.5	10.2	373	2	US-09-990-444-503	Sequence 503, App	218	149.5	9.3	637	2	US-09-569-611C-35	Sequence 35, Appl
146	163.5	10.2	373	2	US-09-997-333-503	Sequence 503, App	219	149.5	9.3	686	3	US-10-162-335-52	Sequence 52, Appl
147	163.5	10.2	373	2	US-09-992-598-503	Sequence 503, App	220	149.5	9.3	7968	3	US-10-077-130-5	Sequence 5, Appl
148	163.5	10.2	373	2	US-10-020-445A-59	Sequence 59, Appl	221	148.5	9.3	686	3	US-10-162-335-48	Sequence 48, Appl
149	163.5	10.2	373	2	US-09-989-735-503	Sequence 503, App	222	148.5	9.3	686	3	US-10-162-335-50	Sequence 50, Appl
150	163.5	10.2	373	2	US-09-978-189-59	Sequence 59, App	223	148.5	9.3	1381	2	US-09-540-245A-16	Sequence 16, Appl
151	163.5	10.2	373	2	US-10-017-085A-59	Sequence 59, Appl	224	148.5	9.3	1381	2	US-10-289-776-16	Sequence 16, Appl
152	163.5	10.2	373	3	US-10-145-129A-59	Sequence 503, App	225	148.5	9.3	1381	3	US-09-191-651-4	Sequence 4, Appl
153	163.5	10.2	373	3	US-09-997-514-503	Sequence 59, Appl	226	148	9.2	344	1	US-08-602-725-34	Sequence 34, Appl
154	163.5	10.2	373	3	US-09-997-514-503	Sequence 59, App	227	148	9.2	357	2	US-09-949-016-9074	Sequence 9074, Ap
155	163.5	10.2	373	3	US-10-013-929A-59	Sequence 59, App	228	148	9.2	363	2	US-09-949-016-11040	Sequence 11040, A
156	163.5	10.2	373	3	US-09-989-728-503	Sequence 503, App	229	148	9.2	365	2	US-09-949-016-9075	Sequence 9075, Ap
157	163.5	10.2	373	3	US-09-997-37A-503	Sequence 59, App	230	148	9.2	407	2	US-09-398-496-6	Sequence 6, Appl
158	163.5	10.2	373	3	US-09-997-653-503	Sequence 503, App	231	148	9.2	407	2	US-09-398-496-6	Sequence 6, Appl
159	163.5	10.2	373	3	US-09-989-293A-503	Sequence 503, App	232	148	9.2	469	2	US-08-753-007A-8	Sequence 8, Appl
160	163.5	10.2	440	2	US-09-866-028-61	Sequence 61, App	233	148	9.2	469	2	US-09-398-496-8	Sequence 8, Appl
161	163.5	10.2	440	2	US-09-944-457-61	Sequence 61, App	234	148	9.2	647	2	US-08-753-007A-32	Sequence 32, Appl
162	163.5	10.2	440	2	US-09-945-584-61	Sequence 61, App	235	148	9.2	647	2	US-09-398-496-32	Sequence 32, Appl
163	163.5	10.2	440	2	US-09-944-944-61	Sequence 61, App	236	148	9.2	647	2	US-08-986-485-2	Sequence 2, Appl
164	163.5	10.2	440	2	US-09-945-587-61	Sequence 61, App	237	146.5	9.1	1101	1	US-08-602-725-32	Sequence 32, Appl
165	163.5	10.2	440	3	US-09-944-884-61	Sequence 61, App	238	146	9.1	464	1	US-09-949-016-6116	Sequence 6116, Ap
166	162.5	10.1	1251	2	US-10-094-749-2841	Sequence 2841, Ap	239	146	9.1	464	2	US-09-949-016-7525	Sequence 7525, Ap
167	162	10.1	805	2	US-08-985-526-34	Sequence 34, Appl	240	146	9.1	1194	2	US-10-191-029-10	Sequence 10, Appl
168	162	10.1	806	1	US-08-443-861-5	Sequence 5, Appl	241	146	9.1	1034	2	US-10-094-749-2631	Sequence 2631, Ap
169	162	10.1	806	1	US-08-193-829B-5	Sequence 5, Appl	242	145.5	9.1	1651	2	US-09-540-245A-18	Sequence 18, Appl
170	162	10.1	806	2	US-09-766-678-5	Sequence 5, Appl	243	145.5	9.1	1651	2	US-10-289-776-18	Sequence 18, Appl
171	162	10.1	1367	1	US-07-813-593-4	Sequence 4, Appl	244	145.5	9.1	1651	2	US-09-191-651-8	Sequence 8, Appl
172	162	10.1					245	145.5	9.1	1651	3		

246	145.5	9.1	1709	2	US-09-949-016-10503	Sequence 10503, A	319	139	8.7	477	1	US-08-286-846A-4	Sequence 4, Appli
247	145	9.0	181	2	US-08-753-007A-4	Sequence 4, Appli	320	139	8.7	477	1	US-08-457-880A-4	Sequence 4, Appli
248	145	9.0	181	2	US-09-398-496-4	Sequence 4, Appli	321	139	8.7	477	1	US-08-444-622A-4	Sequence 4, Appli
249	145	9.0	605	2	US-08-753-007A-2	Sequence 2, Appli	322	139	8.7	477	2	US-08-942-562-4	Sequence 4, Appli
250	145	9.0	605	2	US-09-398-496-2	Sequence 2, Appli	323	139	8.7	477	2	US-09-156-923-4	Sequence 3395, Ap
251	145	9.0	1395	2	US-09-540-245A-15	Sequence 15, Appl	324	139	8.7	650	2	US-10-104-047-3395	Sequence 2, Appli
252	145	9.0	1395	2	US-10-289-776-15	Sequence 15, Appl	325	139	8.7	822	1	US-08-359-705B-2	Sequence 2, Appli
253	145	9.0	1395	3	US-09-191-651-2	Sequence 2, Appli	326	139	8.7	822	1	US-08-286-846A-2	Sequence 2, Appli
254	144.5	9.0	686	3	US-10-162-335-46	Sequence 46, Appl	327	139	8.7	822	1	US-08-457-880A-2	Sequence 2, Appli
255	144.5	9.0	1297	2	US-09-540-245A-17	Sequence 17, Appl	328	139	8.7	822	2	US-08-444-622A-2	Sequence 2, Appli
256	144.5	9.0	1297	3	US-10-289-776-17	Sequence 17, Appl	329	139	8.7	822	2	US-08-942-562-2	Sequence 2, Appli
257	144.5	9.0	1297	3	US-09-191-651-6	Sequence 6, Appli	330	139	8.7	822	2	US-09-156-923-2	Sequence 2, Appli
258	144	9.0	1911	1	US-08-348-006B-5	Sequence 5, Appli	331	139	8.7	822	2	US-09-949-016-6698	Sequence 6698, Ap
259	144	9.0	1911	1	US-08-800-857A-5	Sequence 5, Appli	332	139	8.7	847	1	US-08-286-305A-5	Sequence 5, Appli
260	144	9.0	1911	2	US-09-158-625-5	Sequence 5, Appli	333	139	8.7	847	1	US-08-441-104A-5	Sequence 5, Appli
261	144	9.0	1911	5	PCT-US94-10166-5	Sequence 5, Appli	334	139	8.7	847	1	US-08-440-816A-5	Sequence 5, Appli
262	143.5	8.9	398	2	US-09-778-510-6	Sequence 6, Appli	335	139	8.7	847	2	US-09-417-381A-5	Sequence 2, Appli
263	143.5	8.9	398	2	US-09-307-794A-84	Sequence 84, Appl	336	138.5	8.6	983	2	US-09-412-554A-2	Sequence 2, Appli
264	143.5	8.9	398	2	US-09-305-125A-84	Sequence 84, Appl	337	137	8.5	321	7	5169835-17	Patent No. 5169835
265	143.5	8.9	398	2	US-09-302-775A-84	Sequence 84, Appl	338	136.5	8.5	146	2	US-08-339-578-2	Sequence 2, Appli
266	143.5	8.9	398	2	US-09-306-700-84	Sequence 84, Appl	339	136.5	8.5	821	1	US-08-928-383B-18	Sequence 18, Appl
267	143.5	8.9	398	2	US-09-303-603A-84	Sequence 84, Appl	340	136	8.5	95	2	US-10-012-231A-148	Sequence 148, App
268	143.5	8.9	398	2	US-09-304-920A-84	Sequence 84, Appl	341	136	8.5	500	2	US-10-015-389A-148	Sequence 148, App
269	143.5	8.9	398	2	US-09-305-064-84	Sequence 84, Appl	342	136	8.5	500	2	US-10-006-768A-148	Sequence 148, App
270	143.5	8.9	398	2	US-09-306-618-84	Sequence 84, Appl	343	136	8.5	500	2	US-10-015-393A-148	Sequence 148, App
271	143.5	8.9	398	2	US-09-306-646-84	Sequence 84, Appl	344	136	8.5	500	2	US-10-011-795B-148	Sequence 148, App
272	143.5	8.9	398	2	US-09-306-679A-84	Sequence 84, Appl	345	136	8.5	500	2	US-10-015-393A-148	Sequence 148, App
273	143.5	8.9	398	2	US-09-304-462-84	Sequence 84, Appl	346	136	8.5	500	2	US-10-011-833A-148	Sequence 148, App
274	143.5	8.9	398	2	US-09-302-736A-84	Sequence 84, Appl	347	136	8.5	500	2	US-10-006-041A-148	Sequence 148, App
275	143.5	8.9	398	2	US-09-306-722A-84	Sequence 84, Appl	348	136	8.5	500	2	US-10-012-064A-148	Sequence 148, App
276	143.5	8.9	398	2	US-09-305-449-84	Sequence 84, Appl	349	136	8.5	500	2	US-10-015-392A-148	Sequence 148, App
277	143.5	8.9	398	2	US-09-303-562B-84	Sequence 84, Appl	350	136	8.5	500	3	US-10-011-795B-148	Sequence 148, App
278	143.5	8.9	398	2	US-09-306-679A-84	Sequence 84, Appl	351	136	8.5	500	3	US-10-015-386A-148	Sequence 148, App
279	143.5	8.9	398	3	US-09-307-841-84	Sequence 84, Appl	352	136	8.5	500	3	US-10-012-121A-148	Sequence 148, App
280	143.5	8.9	432	2	US-09-778-510-2	Sequence 2, Appli	353	136	8.5	500	3	US-10-006-485A-148	Sequence 148, App
281	143	8.9	642	1	US-08-217-299-1	Sequence 1, Appli	354	136	8.5	500	3	US-10-006-746A-148	Sequence 148, App
282	143	8.9	698	1	US-08-602-725-36	Sequence 36, Appl	355	136	8.5	500	3	US-10-012-752A-148	Sequence 148, App
283	143	8.9	702	2	US-09-949-016-648A	Sequence 648A, Ap	356	136	8.5	500	3	US-10-017-253A-148	Sequence 148, App
284	143	8.9	734	1	US-08-389-459A-17	Sequence 17, Appl	357	136	8.5	500	3	US-10-015-519A-148	Sequence 148, App
285	143	8.9	734	2	US-08-387-867A-17	Sequence 17, Appl	358	136	8.5	500	3	US-10-015-715A-148	Sequence 148, App
286	143	8.9	740	2	US-09-949-016-8168	Sequence 8168, Ap	359	135	8.4	338	2	US-10-007-236A-148	Sequence 148, App
287	143	8.9	1115	2	US-10-012-231A-58	Sequence 58, Appl	360	134.5	8.4	290	2	US-09-976-594-404	Sequence 404, App
288	143	8.9	1115	2	US-10-015-389A-58	Sequence 58, Appl	361	134.5	8.4	290	2	US-09-910-174B-8	Sequence 8, Appli
289	143	8.9	1115	2	US-10-006-768A-58	Sequence 58, Appl	362	134.5	8.4	290	2	US-09-620-461-8	Sequence 8, Appli
290	143	8.9	1115	2	US-10-015-671A-58	Sequence 58, Appl	363	134.5	8.4	290	2	US-09-451-291-1	Sequence 1, Appli
291	143	8.9	1115	2	US-10-015-393A-58	Sequence 58, Appl	364	134.5	8.4	290	2	US-09-645-069-4	Sequence 4, Appli
292	143	8.9	1115	2	US-10-011-833A-58	Sequence 58, Appl	365	134.5	8.4	290	2	US-09-915-789A-17	Sequence 17, Appl
293	143	8.9	1115	2	US-10-012-064A-58	Sequence 58, Appl	366	134.5	8.4	290	2	US-09-644-934-4	Sequence 4, Appli
294	143	8.9	1115	2	US-10-012-064A-58	Sequence 58, Appl	367	134.5	8.4	290	2	US-09-875-338-2	Sequence 2, Appli
295	143	8.9	1115	2	US-10-015-392A-58	Sequence 58, Appl	368	134.5	8.4	290	3	US-10-115-609-4	Sequence 4, Appli
296	143	8.9	1115	3	US-10-011-795B-58	Sequence 58, Appl	369	134.5	8.4	322	2	US-09-667-135-2	Sequence 2, Appli
297	143	8.9	1115	3	US-10-015-386A-58	Sequence 58, Appl	370	134.5	8.4	322	2	US-09-910-174B-29	Sequence 29, Appl
298	143	8.9	1115	3	US-10-012-121A-58	Sequence 58, Appl	371	134.5	8.4	322	2	US-09-620-461-29	Sequence 29, Appl
299	143	8.9	1115	3	US-10-006-485A-58	Sequence 58, Appl	372	134.5	8.4	483	2	US-09-949-016-8574	Sequence 8574, Ap
300	143	8.9	1115	3	US-10-006-746A-58	Sequence 58, Appl	373	134	8.3	338	1	US-08-414-657D-60	Sequence 60, Appl
301	143	8.9	1115	3	US-10-012-752A-58	Sequence 58, Appl	374	134	8.3	338	2	US-09-135-080-8	Sequence 8, Appli
302	143	8.9	1115	3	US-10-017-253A-58	Sequence 58, Appl	375	134	8.3	771	2	US-08-434-000A-8	Sequence 8, Appli
303	143	8.9	1115	3	US-10-015-519A-58	Sequence 58, Appl	376	134	8.3	771	2	US-09-312-157-8	Sequence 8, Appli
304	143	8.9	1115	3	US-10-015-715A-58	Sequence 58, Appl	377	134	8.3	771	2	US-09-717-888-8	Sequence 8, Appli
305	143	8.9	1115	3	US-10-007-236A-58	Sequence 58, Appl	378	134	8.3	868	1	US-08-374-834-1	Sequence 1, Appli
306	142	8.8	847	2	US-09-949-002-328	Sequence 328, App	379	134	8.3	868	2	US-08-644-271-1	Sequence 1, Appli
307	142	8.8	862	2	US-09-949-002-427	Sequence 427, App	380	134	8.3	868	2	US-09-077-955-1	Sequence 1, Appli
308	140.5	8.8	946	5	PCT-US95-08493-13	Sequence 13, Appl	381	134	8.3	868	2	US-10-016-283-1	Sequence 1, Appli
309	140	8.7	501	1	US-08-408-095-31	Sequence 31, Appl	382	134	8.3	1617	2	US-09-784-358-16	Sequence 16, Appl
310	139.5	8.7	826	2	US-09-877-730-16	Sequence 16, Appl	383	134	8.3	1691	2	US-09-784-358-2	Sequence 2, Appli
311	139.5	8.7	904	2	US-09-877-730-6	Sequence 6, Appli	384	133.5	8.3	278	2	US-09-270-767-42034	Sequence 42034, A
312	139.5	8.7	907	2	US-08-877-730-20	Sequence 20, Appl	385	133.5	8.3	347	2	US-09-667-135-4	Sequence 4, Appli
313	139.5	8.7	985	2	US-09-877-730-10	Sequence 10, Appl	386	133	8.3	310	1	US-08-414-657D-45	Sequence 45, Appl
314	139.5	8.7	991	2	US-09-877-730-12	Sequence 12, Appl	387	133	8.3	338	1	US-08-414-657D-42	Sequence 42, Appl
315	139.5	8.7	1069	2	US-09-877-730-2	Sequence 2, Appli	388	133	8.3	338	1	US-08-414-657D-43	Sequence 43, Appl
316	139.5	8.7	1072	2	US-09-877-730-18	Sequence 18, Appl	389	133	8.3	338	2	US-09-135-080-4	Sequence 4, Appli
317	139.5	8.7	1150	2	US-09-877-730-8	Sequence 8, Appli	390	133	8.3	582	3	US-10-162-335-94	Sequence 94, Appl
318	139	8.7	477	1	US-08-359-705B-4	Sequence 4, Appli	391	133	8.3	894	2	US-09-949-016-10605	Sequence 10605, A

392	132.5	8.3	764	2	US-09-142-956B-14	Sequence 14, Appl	465	129	8.0	769	2	US-08-434-000A-10	Sequence 10, Appl
393	132.5	8.3	767	1	US-08-874-678-2	Sequence 2, Appl	466	129	8.0	769	2	US-09-312-157-10	Sequence 10, Appl
394	132.5	8.3	767	2	US-08-643-839-2	Sequence 2, Appl	467	129	8.0	769	2	US-09-717-888-10	Sequence 10, Appl
395	132.5	8.3	767	2	US-09-348-886-2	Sequence 2, Appl	468	129	8.0	769	2	US-09-818-247-3	Sequence 3, Appl
396	132.5	8.3	767	2	US-10-105-901A-2	Sequence 2, Appl	468	128.5	8.0	757	2	US-09-818-247-2	Sequence 2, Appl
397	132.5	8.3	801	2	US-09-383-630-6	Sequence 6, Appl	469	128.5	8.0	1953	2	US-09-917-254-92	Sequence 92, Appl
398	132.5	8.3	1356	1	US-08-810-116-8	Sequence 8, Appl	470	128	8.0	245	2	US-09-645-063-2	Sequence 2, Appl
399	132.5	8.3	1356	1	US-07-930-548A-8	Sequence 8, Appl	471	128	8.0	245	2	US-09-644-934-2	Sequence 2, Appl
400	132.5	8.3	1356	2	US-09-098-707A-2	Sequence 2, Appl	472	128	8.0	245	2	US-10-115-609-2	Sequence 2, Appl
401	132.5	8.3	1356	2	US-09-483-539-2	Sequence 2, Appl	473	128	8.0	245	3	US-10-163-335-100	Sequence 100, App
402	132.5	8.3	1356	2	US-09-949-016-6198	Sequence 6198, Ap	475	128	8.0	869	1	US-08-374-834-16	Sequence 16, Appl
403	132.5	8.3	1356	2	US-10-100-405A-2	Sequence 2, Appl	476	128	8.0	869	1	US-08-644-271-29	Sequence 29, Appl
404	132.5	8.3	1356	2	US-10-022-939-2	Sequence 2, Appl	477	128	8.0	869	2	US-09-077-955-33	Sequence 33, Appl
405	132.5	8.3	1456	2	US-09-949-016-9853	Sequence 9853, Ap	478	128	8.0	869	2	US-09-715-249-8	Sequence 33, Appl
406	132	8.3	1070	2	US-09-961-403-3	Sequence 3, Appl	479	128	8.0	869	2	US-10-016-283-33	Sequence 33, Appl
407	131.5	8.2	303	2	US-09-651-200-23	Sequence 23, Appl	480	128	8.0	1363	2	US-09-375-248-19	Sequence 19, Appl
408	131.5	8.2	303	2	US-09-441-411-15	Sequence 15, Appl	481	127	7.9	504	2	US-09-949-016-7020	Sequence 7020, Ap
409	131.5	8.2	303	2	US-09-441-411-20	Sequence 20, Appl	482	127	7.9	504	2	US-09-991-181-119	Sequence 119, App
410	131.5	8.2	309	1	US-08-456-104-4	Sequence 4, Appl	483	127	7.9	504	2	US-09-990-444-119	Sequence 119, App
411	131.5	8.2	309	2	US-08-479-744A-23	Sequence 23, Appl	484	127	7.9	504	2	US-09-997-333-119	Sequence 119, App
412	131.5	8.2	309	2	US-08-280-757B-23	Sequence 23, Appl	485	127	7.9	504	2	US-09-992-598-119	Sequence 119, App
413	131.5	8.2	309	2	US-08-205-697A-21	Sequence 21, Appl	486	127	7.9	504	2	US-09-989-735-119	Sequence 119, App
414	131.5	8.2	309	2	US-08-702-525-21	Sequence 21, Appl	487	127	7.9	504	3	US-09-989-726-119	Sequence 119, App
415	131.5	8.2	309	2	US-09-651-200-22	Sequence 22, Appl	488	127	7.9	504	3	US-09-997-514-119	Sequence 119, App
416	131.5	8.2	309	2	US-09-667-135-33	Sequence 33, Appl	489	127	7.9	504	3	US-09-989-728-119	Sequence 119, App
417	131.5	8.2	309	2	US-09-425-762-23	Sequence 23, Appl	490	127	7.9	504	3	US-09-997-653-119	Sequence 119, App
418	131.5	8.2	309	2	US-09-837-867A-21	Sequence 21, Appl	491	127	7.9	504	3	US-09-997-653-119	Sequence 119, App
419	131.5	8.2	309	2	US-09-206-132-4	Sequence 4, Appl	492	127	7.9	504	3	US-09-989-293A-119	Sequence 119, App
420	131.5	8.2	309	2	US-09-441-411-13	Sequence 13, Appl	493	127	7.9	511	2	US-09-949-016-10054	Sequence 10054, A
421	131.5	8.2	309	2	US-09-441-411-18	Sequence 18, Appl	494	126.5	7.9	306	1	US-08-147-772-4	Sequence 4, Appl
422	131.5	8.2	309	2	US-09-441-411-24	Sequence 24, Appl	495	126.5	7.9	306	1	US-08-456-104-8	Sequence 8, Appl
423	131.5	8.2	309	2	US-09-425-516-23	Sequence 23, Appl	496	126.5	7.9	306	1	US-08-101-624-25	Sequence 25, Appl
424	131.5	8.2	309	5	PCT-US95-02576-21	Sequence 21, Appl	497	126.5	7.9	306	2	US-08-153-262-4	Sequence 4, Appl
425	131.5	8.2	313	2	US-09-700-397-4	Sequence 4, Appl	498	126.5	7.9	306	2	US-08-479-744A-31	Sequence 31, Appl
426	131.5	8.2	314	2	US-08-205-697A-13	Sequence 13, Appl	499	126.5	7.9	306	2	US-08-280-757B-31	Sequence 31, Appl
427	131.5	8.2	314	2	US-08-702-525-13	Sequence 13, Appl	500	126.5	7.9	306	2	US-09-159-135-4	Sequence 4, Appl
428	131.5	8.2	314	2	US-09-837-867A-13	Sequence 13, Appl	501	126.5	7.9	306	2	US-08-205-697A-17	Sequence 17, Appl
429	131.5	8.2	314	2	US-09-441-411-14	Sequence 14, Appl	502	126.5	7.9	306	2	US-08-702-525-17	Sequence 17, Appl
430	131.5	8.2	314	2	US-09-441-411-19	Sequence 19, Appl	503	126.5	7.9	306	2	US-09-450-798-4	Sequence 4, Appl
431	131.5	8.2	314	5	PCT-US95-02576-13	Sequence 13, Appl	504	126.5	7.9	306	2	US-09-651-200-17	Sequence 17, Appl
432	131.5	8.2	344	2	US-09-700-397-3	Sequence 3, Appl	505	126.5	7.9	306	2	US-09-667-135-35	Sequence 35, Appl
433	131.5	8.2	344	2	US-09-999-833A-523	Sequence 523, App	506	126.5	7.9	306	2	US-09-425-762-31	Sequence 31, Appl
434	131.5	8.2	344	2	US-10-020-445A-523	Sequence 523, App	507	126.5	7.9	306	2	US-09-837-867A-17	Sequence 17, Appl
435	131.5	8.2	344	2	US-09-978-189-523	Sequence 523, App	508	126.5	7.9	306	2	US-08-453-386A-4	Sequence 4, Appl
436	131.5	8.2	344	2	US-10-017-085A-523	Sequence 523, App	509	126.5	7.9	306	2	US-09-206-132-8	Sequence 8, Appl
437	131.5	8.2	344	3	US-10-145-128A-523	Sequence 523, App	510	126.5	7.9	306	2	US-09-425-516-31	Sequence 31, Appl
438	131.5	8.2	344	3	US-10-013-929A-523	Sequence 523, App	511	126.5	7.9	306	5	PCT-US95-02576-17	Sequence 17, Appl
439	131.5	8.2	344	3	US-10-013-917A-523	Sequence 523, App	512	126.5	7.9	1447	5	PCT-US94-05277-2	Sequence 2, Appl
440	131.5	8.2	356	2	US-09-441-411-11	Sequence 11, Appl	513	126.5	7.9	1447	5	PCT-US94-05277-2	Sequence 2, Appl
441	131.5	8.2	356	2	US-09-441-411-12	Sequence 12, Appl	514	126	7.9	758	1	US-08-874-678-1	Sequence 1, Appl
442	131.5	8.2	356	2	US-09-441-411-16	Sequence 16, Appl	515	126	7.9	758	1	US-08-643-839-1	Sequence 1, Appl
443	131.5	8.2	356	2	US-09-441-411-17	Sequence 17, Appl	516	126	7.9	758	2	US-09-051-363-24	Sequence 24, Appl
444	131.5	8.2	668	1	US-08-232-538-13	Sequence 13, Appl	517	126	7.9	758	2	US-09-348-886-1	Sequence 1, Appl
445	131.5	8.2	668	1	US-08-786-164-13	Sequence 13, Appl	518	126	7.9	758	2	US-10-105-901A-1	Sequence 1, Appl
446	131.5	8.2	788	1	US-08-232-538-15	Sequence 15, Appl	519	126	7.9	758	2	US-09-499-468-39	Sequence 39, Appl
447	131.5	8.2	788	1	US-08-786-164-15	Sequence 15, Appl	520	126	7.9	780	1	US-08-232-538-14	Sequence 14, Appl
448	131	8.2	252	2	US-09-270-767-4627	Sequence 4627, A	521	126	7.9	780	1	US-08-786-164-14	Sequence 14, Appl
449	131	8.2	771	2	US-09-818-247-4	Sequence 4, Appl	522	126	7.9	1338	2	US-08-750-141A-3	Sequence 3, Appl
450	130.5	8.1	191	2	US-09-270-767-33678	Sequence 33678, A	523	126	7.9	1338	2	US-09-119-014D-6	Sequence 6, Appl
451	130.5	8.1	191	2	US-09-270-767-48895	Sequence 48895, A	524	126	7.9	2596	2	US-09-548-473B-6	Sequence 6, Appl
452	130.5	8.1	284	3	US-09-191-651-10	Sequence 10, Appl	525	126	7.9	2630	3	US-10-077-130-2	Sequence 2, Appl
453	130.5	8.1	434	2	US-09-540-245A-19	Sequence 19, Appl	526	125.5	7.8	227	2	US-09-205-258-947	Sequence 947, App
454	130.5	8.1	434	2	US-10-289-776-19	Sequence 776-19	527	125.5	7.8	227	2	US-10-004-860-947	Sequence 947, App
455	129.5	8.1	252	1	US-08-414-657D-56	Sequence 56, Appl	528	125.5	7.8	230	7	5169835-13	Patent No. 5169835
456	129.5	8.1	252	1	US-08-414-657D-57	Sequence 57, Appl	529	125.5	7.8	282	2	US-09-667-857-393	Sequence 393, App
457	129.5	8.1	287	1	US-08-414-657D-48	Sequence 48, Appl	530	125.5	7.8	282	2	US-09-667-857-393	Sequence 393, App
458	129.5	8.1	287	1	US-08-414-657D-49	Sequence 49, Appl	531	125.5	7.8	282	2	US-10-198-053-393	Sequence 393, App
459	129.5	8.1	304	1	US-08-414-657D-44	Sequence 44, Appl	532	125.5	7.8	282	2	US-09-915-789A-5	Sequence 5, Appl
460	129.5	8.1	308	1	US-08-414-657D-46	Sequence 46, Appl	533	125.5	7.8	282	2	US-09-991-181-291	Sequence 291, App
461	129.5	8.1	315	1	US-08-414-657D-47	Sequence 47, Appl	534	125.5	7.8	282	2	US-09-929-769-8	Sequence 8, Appl
462	129.5	8.1	325	1	US-08-414-657D-2	Sequence 2, Appl	535	125.5	7.8	282	2	US-09-990-444-291	Sequence 291, App
463	129.5	8.1	325	1	US-08-414-657D-41	Sequence 41, Appl	536	125.5	7.8	282	2	US-09-997-333-291	Sequence 291, App
464	129.5	8.1	325	2	US-09-135-080-2	Sequence 2, Appl	537	125.5	7.8	282	2	US-09-992-598-291	Sequence 291, App

538	125.5	7.8	282	2	US-09-827-271-393	Sequence 333, App	611	121	7.5	622	2	US-09-499-846-2	Sequence 2, Appli
539	125.5	7.8	282	2	US-09-989-735-291	Sequence 231, App	612	121	7.5	643	1	US-08-471-570-6	Sequence 6, Appli
540	125.5	7.8	282	3	US-09-989-726-291	Sequence 291, App	613	121	7.5	769	1	US-08-471-570-8	Sequence 8, Appli
541	125.5	7.8	282	3	US-09-997-514-291	Sequence 291, App	614	121	7.5	820	1	US-07-921-807B-3	Sequence 3, Appli
542	125.5	7.8	282	3	US-09-989-728-291	Sequence 291, App	615	121	7.5	820	1	US-08-441-944A-3	Sequence 3, Appli
543	125.5	7.8	282	3	US-09-997-349-291	Sequence 291, App	616	121	7.5	820	1	US-08-166-717D-6	Sequence 6, Appli
544	125.5	7.8	282	3	US-09-997-653-291	Sequence 291, App	617	121	7.5	820	2	US-08-439-952A-1	Sequence 1, Appli
545	125.5	7.8	282	3	US-09-989-293A-291	Sequence 291, App	618	120.5	7.5	821	2	US-08-451-822A-13	Sequence 13, Appli
546	125.5	7.8	309	2	US-09-404-879A-392	Sequence 392, App	619	120.5	7.5	821	2	US-08-323-430-13	Sequence 13, Appli
547	125.5	7.8	309	2	US-09-667-857-392	Sequence 392, App	620	120	7.5	821	2	US-09-254-465A-2	Sequence 2, Appli
548	125.5	7.8	309	2	US-10-198-053-392	Sequence 392, App	621	120	7.5	321	2	US-09-953-499-2	Sequence 2, Appli
549	125.5	7.8	309	2	US-09-827-271-392	Sequence 392, App	622	120	7.5	321	2	US-09-999-833A-52	Sequence 52, Appli
550	125.5	7.8	480	2	US-09-875-338-5	Sequence 5, Appli	623	120	7.5	321	2	US-10-020-445A-52	Sequence 52, Appli
551	125.5	7.8	558	2	US-09-667-135-31	Sequence 31, Appl	624	120	7.5	321	2	US-09-978-189-52	Sequence 52, Appli
552	125.5	7.8	795	2	US-09-949-016-7119	Sequence 7119, Ap	625	120	7.5	321	2	US-10-017-085A-52	Sequence 52, Appli
553	125.5	7.8	806	2	US-09-383-630-3	Sequence 3, Appli	626	120	7.5	321	3	US-10-145-129A-52	Sequence 52, Appli
554	125	7.8	478	5	PCT-US95-08493-15	Sequence 15, Appl	627	120	7.5	321	3	US-10-013-929A-52	Sequence 52, Appli
555	125	7.8	833	2	US-09-949-016-11496	Sequence 11496, A	628	120	7.5	321	3	US-10-013-917A-52	Sequence 52, Appli
556	125	7.8	860	5	PCT-US95-08493-19	Sequence 19, Appl	629	120	7.5	609	2	US-09-949-016-7747	Sequence 7747, Ap
557	125	7.8	868	5	PCT-US95-08493-21	Sequence 21, Appl	630	120	7.5	609	2	US-09-949-016-7749	Sequence 7749, Ap
558	125	7.8	1180	2	US-09-949-016-6577	Sequence 6577, Ap	631	120	7.5	609	2	US-09-949-016-7750	Sequence 7750, Ap
559	124.5	7.8	1241	2	US-09-040-774-2	Sequence 2, Appli	632	120	7.5	609	2	US-09-949-016-7751	Sequence 7751, Ap
560	124.5	7.8	1665	2	US-09-858-664A-2	Sequence 2, Appli	633	120	7.5	609	2	US-09-949-016-7752	Sequence 7752, Ap
561	124.5	7.8	1665	2	US-10-274-978-2	Sequence 2, Appli	634	120	7.5	609	2	US-09-949-016-7753	Sequence 7753, Ap
562	124.5	7.8	1665	2	US-10-697-263-2	Sequence 2, Appli	635	120	7.5	609	2	US-09-949-016-7754	Sequence 7754, Ap
563	124	7.7	462	1	US-08-752-307B-7	Sequence 7, Appli	636	120	7.5	609	2	US-09-949-016-7754	Sequence 7754, Ap
564	124	7.7	462	2	US-09-707-802-7	Sequence 7, Appli	637	120	7.5	817	1	US-07-640-029-2	Sequence 2, Appli
565	124	7.7	462	2	US-09-931-326-7	Sequence 7, Appli	638	120	7.5	822	1	US-07-997-133-1	Sequence 1, Appli
566	124	7.7	465	1	US-08-752-307B-5	Sequence 5, Appli	639	120	7.5	822	1	US-07-921-807B-4	Sequence 4, Appli
567	124	7.7	465	2	US-09-707-802-5	Sequence 5, Appli	640	120	7.5	822	1	US-08-459-296-2	Sequence 2, Appli
568	124	7.7	465	2	US-09-991-326-5	Sequence 5, Appli	641	120	7.5	822	1	US-08-441-944A-4	Sequence 4, Appli
569	124	7.7	596	1	US-08-752-307B-13	Sequence 13, Appl	642	120	7.5	822	1	US-08-451-822A-12	Sequence 12, Appl
570	124	7.7	596	2	US-09-707-802-13	Sequence 13, Appl	643	120	7.5	822	2	US-08-439-992A-2	Sequence 2, Appli
571	124	7.7	596	2	US-09-991-326-13	Sequence 13, Appl	644	120	7.5	822	2	US-08-323-430-12	Sequence 12, Appli
572	124	7.7	612	1	US-08-752-307B-11	Sequence 11, Appl	645	120	7.5	822	2	US-09-620-561-2	Sequence 2, Appli
573	124	7.7	612	2	US-09-707-802-11	Sequence 11, Appl	646	120	7.5	1018	1	US-08-452-052-2	Sequence 2, Appli
574	124	7.7	612	2	US-09-991-326-11	Sequence 11, Appl	647	120	7.5	1745	2	US-09-800-729-89	Sequence 89, Appli
575	124	7.7	1268	2	US-08-506-296B-28	Sequence 28, Appl	648	119.5	7.4	227	2	US-09-915-789A-19	Sequence 19, Appl
576	123.5	7.7	59	2	US-09-324-541-2	Sequence 2, Appli	649	119.5	7.4	816	1	US-07-640-029-1	Sequence 1, Appli
577	123.5	7.7	282	2	US-10-198-053-623	Sequence 623, App	650	119.5	7.4	1610	1	US-09-548-473B-4	Sequence 4, Appli
578	123.5	7.7	299	2	US-09-651-200-15	Sequence 15, Appl	651	119	7.4	291	2	US-10-027-736A-19	Sequence 19, Appl
579	123.5	7.7	322	2	US-09-383-586-33	Sequence 33, Appl	652	119	7.4	302	2	US-09-877-730-14	Sequence 14, Appl
580	123.5	7.7	322	2	US-09-823-038A-33	Sequence 33, Appl	653	119	7.4	315	2	US-09-949-016-11121	Sequence 11121, A
581	123.5	7.7	419	7	5169835-2	Patent No. 5169835	654	119	7.4	315	2	US-09-949-016-11122	Sequence 11122, A
582	123.5	7.7	757	2	US-08-434-000A-6	Sequence 6, Appli	655	119	7.4	380	2	US-09-877-730-4	Sequence 4, Appli
583	123.5	7.7	757	2	US-09-312-157-6	Sequence 6, Appli	656	119	7.4	440	2	US-08-759-628-4	Sequence 4, Appli
584	123.5	7.7	757	2	US-09-717-888-6	Sequence 6, Appli	657	119	7.4	985	2	US-09-999-833A-211	Sequence 211, App
585	123	7.7	302	2	US-09-915-789A-18	Sequence 18, Appl	658	119	7.4	985	2	US-10-020-445A-211	Sequence 211, App
586	123	7.7	309	2	US-09-667-135-6	Sequence 6, Appli	659	119	7.4	985	2	US-09-978-189-211	Sequence 211, App
587	123	7.7	309	2	US-09-910-174B-7	Sequence 7, Appli	660	119	7.4	985	3	US-10-017-085A-211	Sequence 211, App
588	123	7.7	309	2	US-09-620-461-7	Sequence 7, Appli	661	119	7.4	985	3	US-10-145-129A-211	Sequence 211, App
589	123	7.7	315	2	US-09-910-174B-28	Sequence 28, Appl	662	119	7.4	985	3	US-10-013-929A-211	Sequence 211, App
590	123	7.7	315	2	US-09-620-461-28	Sequence 28, Appl	663	119	7.4	985	3	US-10-013-917A-211	Sequence 211, App
591	123	7.7	526	1	US-08-471-570-4	Sequence 4, Appli	664	119	7.4	1007	3	US-10-329-258-23	Sequence 23, Appl
592	123	7.7	607	1	US-08-752-307B-12	Sequence 12, Appl	665	119	7.4	1018	1	US-08-408-093-6	Sequence 6, Appli
593	123	7.7	607	2	US-09-707-802-12	Sequence 12, Appl	666	119	7.4	1018	1	US-08-408-420A-6	Sequence 6, Appli
594	123	7.7	607	2	US-09-991-326-12	Sequence 12, Appl	667	119	7.4	1018	1	US-08-714-901-6	Sequence 6, Appli
595	123	7.7	652	1	US-08-471-570-10	Sequence 10, Appl	668	119	7.4	1018	2	US-08-040-741-6	Sequence 6, Appli
596	123	7.7	1091	2	US-08-986-485-5	Sequence 5, Appli	669	119	7.4	1044	2	US-09-949-016-10321	Sequence 10321, A
597	122.5	7.6	1311	1	US-08-340-011-5	Sequence 5, Appli	670	118.5	7.4	252	2	US-10-027-736A-68	Sequence 68, Appl
598	122.5	7.6	1311	2	US-08-901-710-5	Sequence 5, Appli	671	118.5	7.4	294	2	US-10-027-736A-18	Sequence 18, Appl
599	122.5	7.6	1311	2	US-09-169-079-5	Sequence 5, Appli	672	118.5	7.4	307	1	US-08-332-562A-83	Sequence 83, Appl
600	122.5	7.6	1311	3	US-09-765-534B-5	Sequence 5, Appli	673	118.5	7.4	315	2	US-09-949-016-7014	Sequence 7014, Ap
601	122.5	7.6	1311	2	US-08-956-991-11	Sequence 11, Appl	674	118.5	7.4	317	2	US-10-027-736A-16	Sequence 16, Appl
602	122.5	7.6	1910	2	US-08-956-991-2	Sequence 2, Appli	675	118.5	7.4	355	1	US-08-471-570-14	Sequence 14, Appl
603	122	7.6	732	2	US-09-818-247-5	Sequence 5, Appli	676	118.5	7.4	471	2	US-09-949-016-9042	Sequence 9042, Ap
604	122	7.6	820	2	US-09-620-561-1	Sequence 1, Appli	677	118.5	7.4	471	2	US-09-949-016-9043	Sequence 9043, Ap
605	121.5	7.6	304	2	US-09-646-561-2	Sequence 2, Appli	678	118.5	7.4	471	2	US-09-949-016-9044	Sequence 9044, Ap
606	121.5	7.6	424	7	5169835-6	Patent No. 5169835	679	118.5	7.4	471	2	US-09-949-016-9045	Sequence 9045, Ap
607	121.5	7.6	828	1	US-08-261-304-2	Sequence 2, Appli	680	118.5	7.4	471	2	US-09-949-016-9046	Sequence 9046, Ap
608	121	7.5	61	2	US-09-513-999C-6595	Sequence 6595, Ap	681	118.5	7.4	471	2	US-09-949-016-9047	Sequence 9047, Ap
609	121	7.5	351	5	PCT-US93-05703-2	Sequence 2, Appli	682	118.5	7.4	471	2	US-09-949-016-9048	Sequence 9048, Ap
610	121	7.5	490	2	US-09-667-135-28	Sequence 28, Appl	683	118.5	7.4	471	2	US-09-949-016-9049	Sequence 9049, Ap

684	118.5	7.4	471	2	US-09-949-016-9050	Sequence 9050, Ap	757	116	7.2	310	2	US-10-027-736A-15	Sequence 15, Appl
685	118.5	7.4	471	2	US-09-949-016-9051	Sequence 9051, Ap	758	116	7.2	332	2	US-09-991-181-517	Sequence 517, App
686	118.5	7.4	646	2	US-09-949-016-9078	Sequence 6728, Ap	759	116	7.2	332	2	US-09-999-833A-216	Sequence 216, App
687	118.5	7.4	646	2	US-09-949-016-9078	Sequence 4, Appl	760	116	7.2	332	2	US-09-990-444-517	Sequence 517, App
688	118.5	7.4	735	5	PCT-US93-00031-13	Sequence 13, Appl	761	116	7.2	332	2	US-09-997-333-517	Sequence 517, App
689	118.5	7.4	735	5	PCT-US93-00031-15	Sequence 15, Appl	762	116	7.2	332	2	US-09-992-598-517	Sequence 517, App
690	118.5	7.4	739	5	PCT-US93-00031-9	Sequence 9, Appl	763	116	7.2	332	2	US-10-020-445A-216	Sequence 216, App
691	118.5	7.4	739	5	PCT-US93-00031-9	Sequence 6, Appl	764	116	7.2	332	2	US-09-989-735-517	Sequence 517, App
692	118.5	7.4	740	5	PCT-US93-00031-17	Sequence 17, Appl	765	116	7.2	332	2	US-09-978-189-216	Sequence 216, App
693	118.5	7.4	1059	2	US-09-907-794A-290	Sequence 290, App	766	116	7.2	332	2	US-10-017-085A-216	Sequence 216, App
694	118.5	7.4	1059	2	US-09-905-125A-290	Sequence 290, App	767	116	7.2	332	3	US-09-989-726-517	Sequence 517, App
695	118.5	7.4	1059	2	US-09-902-775A-290	Sequence 290, App	768	116	7.2	332	3	US-10-145-129A-216	Sequence 216, App
696	118.5	7.4	1059	2	US-09-906-700-290	Sequence 290, App	769	116	7.2	332	3	US-09-997-514-517	Sequence 517, App
697	118.5	7.4	1059	2	US-09-903-603A-290	Sequence 290, App	770	116	7.2	332	3	US-10-013-929A-216	Sequence 216, App
698	118.5	7.4	1059	2	US-09-904-920A-290	Sequence 290, App	771	116	7.2	332	3	US-09-989-728-517	Sequence 517, App
699	118.5	7.4	1059	2	US-09-909-064-290	Sequence 290, App	772	116	7.2	332	3	US-10-013-917A-216	Sequence 216, App
700	118.5	7.4	1059	2	US-09-905-381A-290	Sequence 290, App	773	116	7.2	332	3	US-09-997-349-517	Sequence 517, App
701	118.5	7.4	1059	2	US-09-906-618-290	Sequence 290, App	774	116	7.2	332	3	US-09-997-653-517	Sequence 517, App
702	118.5	7.4	1059	2	US-09-906-646-290	Sequence 290, App	775	116	7.2	332	3	US-09-989-293A-517	Sequence 517, App
703	118.5	7.4	1059	2	US-09-904-462-290	Sequence 290, App	776	116	7.2	1509	2	US-09-677-046A-2	Sequence 2, Appl
704	118.5	7.4	1059	2	US-09-902-736A-290	Sequence 290, App	777	115.5	7.2	63	2	US-10-037-417-128	Sequence 128, App
705	118.5	7.4	1059	2	US-09-906-722A-290	Sequence 290, App	778	115.5	7.2	288	2	US-09-651-200-14	Sequence 14, Appl
706	118.5	7.4	1059	2	US-09-905-449-290	Sequence 290, App	779	115.5	7.2	320	2	US-08-205-697A-2	Sequence 2, Appl
707	118.5	7.4	1059	2	US-09-903-562B-290	Sequence 290, App	780	115.5	7.2	320	2	US-08-702-525-2	Sequence 2, Appl
708	118.5	7.4	1059	2	US-09-906-679A-290	Sequence 290, App	781	115.5	7.2	320	2	US-09-837-867A-2	Sequence 2, Appl
709	118.5	7.4	1059	3	US-09-907-841-290	Sequence 290, App	782	115.5	7.2	320	5	PCT-US95-02576-2	Sequence 2, Appl
710	118.5	7.4	1119	2	US-09-907-794A-294	Sequence 294, App	783	115.5	7.2	513	2	US-09-910-174B-18	Sequence 18, Appl
711	118.5	7.4	1119	2	US-09-905-125A-294	Sequence 294, App	784	115.5	7.2	513	2	US-09-620-461-18	Sequence 18, Appl
712	118.5	7.4	1119	2	US-09-902-775A-294	Sequence 294, App	785	115.5	7.2	514	2	US-09-949-016-11380	Sequence 11380, A
713	118.5	7.4	1119	2	US-09-906-700-294	Sequence 294, App	786	115.5	7.2	517	2	US-09-723-368-4	Sequence 4, Appl
714	118.5	7.4	1119	2	US-09-906-646-294	Sequence 294, App	787	115.5	7.2	608	2	US-09-095-385-4	Sequence 4, Appl
715	118.5	7.4	1119	2	US-09-903-603A-294	Sequence 294, App	788	115.5	7.2	662	1	US-08-261-304-7	Sequence 7, Appl
716	118.5	7.4	1119	2	US-09-909-064-294	Sequence 294, App	789	115.5	7.2	888	1	US-08-445-640-35	Sequence 35, Appl
717	118.5	7.4	1119	2	US-09-905-381A-294	Sequence 294, App	790	115.5	7.2	888	2	US-08-170-558-35	Sequence 35, Appl
718	118.5	7.4	1119	2	US-09-906-618-294	Sequence 294, App	791	115.5	7.2	888	2	US-08-447-314-35	Sequence 35, Appl
719	118.5	7.4	1119	2	US-09-906-646-294	Sequence 294, App	792	115.5	7.2	888	2	US-08-445-461-35	Sequence 35, Appl
720	118.5	7.4	1119	2	US-09-904-462-294	Sequence 294, App	793	115.5	7.2	888	2	US-09-223-490-35	Sequence 35, Appl
721	118.5	7.4	1119	2	US-09-902-736A-294	Sequence 294, App	794	115.5	7.2	888	3	US-10-646-760-35	Sequence 35, Appl
722	118.5	7.4	1119	2	US-09-906-722A-294	Sequence 294, App	795	115	7.2	220	2	US-09-915-789A-23	Sequence 23, Appl
723	118.5	7.4	1119	2	US-09-905-449-294	Sequence 294, App	796	115	7.2	261	2	US-09-270-767-32898	Sequence 32898, A
724	118.5	7.4	1119	2	US-09-903-562B-294	Sequence 294, App	797	115	7.2	261	2	US-09-270-767-48115	Sequence 48115, A
725	118.5	7.4	1119	2	US-09-906-679A-294	Sequence 294, App	798	115	7.2	354	7	5169835-4	Patent No. 5169835
726	118.5	7.4	1119	3	US-09-907-841-294	Sequence 294, App	799	115	7.2	549	2	US-09-858-668A-5	Sequence 5, Appl
727	118.5	7.4	1248	2	US-09-949-016-10595	Sequence 10595, A	800	115	7.2	549	2	US-10-274-978-6	Sequence 6, Appl
728	118.5	7.4	1248	2	US-09-949-016-10596	Sequence 10596, A	801	115	7.2	549	2	US-10-697-263-6	Sequence 6, Appl
729	118	7.4	272	1	US-08-282-951-6	Sequence 6, Appl	802	115	7.2	602	1	US-08-428-926-5	Sequence 5, Appl
730	118	7.4	337	1	US-08-442-043A-18	Sequence 18, Appl	803	115	7.2	602	1	US-08-428-927-5	Sequence 5, Appl
731	118	7.4	337	2	US-09-560-639-6	Sequence 6, Appl	804	115	7.2	602	1	US-08-428-298-5	Sequence 5, Appl
732	118	7.4	337	2	US-08-441-893A-18	Sequence 18, Appl	805	115	7.2	602	1	US-08-339-517-5	Sequence 5, Appl
733	118	7.4	342	2	US-09-032-337-41	Sequence 41, Appl	806	115	7.2	611	1	US-08-752-307B-10	Sequence 10, Appl
734	118	7.4	421	3	US-10-162-335-96	Sequence 96, Appl	807	115	7.2	611	2	US-09-707-802-10	Sequence 10, Appl
735	118	7.4	421	3	US-10-162-335-98	Sequence 98, Appl	808	115	7.2	611	2	US-09-991-326-10	Sequence 10, Appl
736	118	7.4	567	2	US-09-560-639-7	Sequence 7, Appl	809	115	7.2	1253	2	US-08-506-296B-14	Sequence 14, Appl
737	118	7.4	567	2	US-09-173-151A-24	Sequence 24, Appl	810	115	7.2	1298	1	US-08-222-616-33	Sequence 33, Appl
738	118	7.4	567	2	US-09-032-337-39	Sequence 39, Appl	811	115	7.2	1298	1	US-08-340-011-2	Sequence 2, Appl
739	117	7.3	241	2	US-09-915-789A-11	Sequence 11, Appl	812	115	7.2	1298	2	US-08-901-710-2	Sequence 2, Appl
740	117	7.3	292	2	US-09-800-729-175	Sequence 175, Appl	813	115	7.2	1298	2	US-08-446-648-33	Sequence 33, Appl
741	117	7.3	316	2	US-10-027-736A-17	Sequence 17, Appl	814	115	7.2	1298	2	US-09-982-610-33	Sequence 33, Appl
742	117	7.3	816	2	US-09-949-016-8119	Sequence 8119, Ap	815	115	7.2	1298	2	US-09-169-079-2	Sequence 2, Appl
743	116.5	7.3	63	2	US-09-397-243D-8	Sequence 8, Appl	816	115	7.2	1298	3	US-09-765-534B-2	Sequence 2, Appl
744	116.5	7.3	195	2	US-10-094-749-3032	Sequence 10, Appl	817	115	7.2	1298	5	PCT-US95-04228-33	Sequence 33, Appl
745	116.5	7.3	212	2	US-09-949-016-10458	Sequence 1032, Ap	818	115	7.2	1362	1	US-08-874-678-33	Sequence 33, Appl
746	116.5	7.3	623	2	US-09-949-016-11206	Sequence 11206, A	819	115	7.2	1362	2	US-08-643-839-33	Sequence 33, Appl
747	116.5	7.3	646	2	US-09-653-961-2	Sequence 2, Appl	820	115	7.2	1362	2	US-09-348-886-33	Sequence 33, Appl
748	116.5	7.3	746	2	US-08-434-000A-4	Sequence 4, Appl	821	115	7.2	1362	2	US-10-105-901A-33	Sequence 33, Appl
749	116.5	7.3	746	2	US-09-312-157-4	Sequence 4, Appl	822	115	7.2	1363	1	US-08-340-011-4	Sequence 4, Appl
750	116.5	7.3	746	2	US-09-717-888-4	Sequence 4, Appl	823	115	7.2	1363	2	US-08-901-710-4	Sequence 4, Appl
751	116.5	7.3	764	2	US-09-949-016-6254	Sequence 6254, Ap	824	115	7.2	1363	2	US-09-375-248-2	Sequence 2, Appl
752	116.5	7.3	764	2	US-09-818-247-1	Sequence 1, Appl	825	115	7.2	1363	2	US-09-169-079-4	Sequence 4, Appl
753	116.5	7.3	1123	2	US-09-949-016-6230	Sequence 6230, Ap	826	115	7.2	1363	3	US-09-765-534B-4	Sequence 4, Appl
754	116.5	7.3	1128	2	US-09-949-016-7522	Sequence 7522, Ap	827	115	7.2	1368	1	US-08-874-678-34	Sequence 34, Appl
755	116.5	7.3	1266	2	US-08-506-296B-4	Sequence 4, Appl	828	115	7.2	1368	2	US-08-643-839-34	Sequence 34, Appl
756	116.5	7.3					829	115	7.2	1368	2	US-09-348-886-34	Sequence 34, Appl

830	115	7.2	1368	2	US-10-105-901A-34	Sequence 34, Appl	903	112.5	7.0	569	2	US-08-411-295F-163	Sequence 163, App
831	114.5	7.1	1363	1	US-08-874-678-32	Sequence 32, Appl	904	112.5	7.0	601	2	US-08-470-335-233	Sequence 233, App
832	114.5	7.1	1363	2	US-08-643-839-32	Sequence 32, Appl	905	112.5	7.0	601	2	US-08-467-602-323	Sequence 323, App
833	114.5	7.1	1363	2	US-09-348-886-32	Sequence 32, Appl	906	112.5	7.0	601	2	US-08-411-295F-249	Sequence 249, App
834	114.5	7.1	1363	2	US-10-105-901A-32	Sequence 32, Appl	907	112.5	7.0	616	2	US-08-467-602-238	Sequence 238, App
835	114	7.1	253	3	US-09-971-543-2	Sequence 2, Appl	908	112.5	7.0	616	2	US-08-411-295F-164	Sequence 164, App
836	114	7.1	969	2	US-09-949-016-8059	Sequence 8059, Ap	909	112.5	7.0	635	2	US-08-467-602-365	Sequence 365, App
837	114	7.1	1260	2	US-08-506-296B-21	Sequence 21, Appl	910	112.5	7.0	635	2	US-08-411-295F-291	Sequence 291, App
838	113.5	7.1	282	2	US-10-027-736A-66	Sequence 66, Appl	911	112.5	7.0	818	2	US-09-684-708A-21	Sequence 21, Appl
839	113.5	7.1	386	2	US-08-467-602-281	Sequence 281, Appl	912	112.5	7.0	818	2	US-08-470-335-234	Sequence 234, App
840	113.5	7.1	386	2	US-08-411-295F-207	Sequence 207, App	913	112.5	7.0	818	2	US-08-467-602-321	Sequence 321, App
841	113.5	7.1	417	2	US-09-949-016-6729	Sequence 6729, Ap	914	112.5	7.0	818	2	US-08-411-295F-247	Sequence 247, App
842	113.5	7.1	456	2	US-09-949-016-7564	Sequence 7564, Ap	915	112.5	7.0	852	2	US-08-467-602-363	Sequence 363, App
843	113.5	7.1	602	1	US-08-168-091A-2	Sequence 2, Appl	916	112.5	7.0	852	2	US-08-411-295F-289	Sequence 289, App
844	113.5	7.1	603	2	US-08-467-602-279	Sequence 279, App	917	112.5	7.0	865	2	US-08-470-335-235	Sequence 235, App
845	113.5	7.1	603	2	US-08-411-295F-205	Sequence 205, App	918	112.5	7.0	865	2	US-08-467-602-322	Sequence 322, App
846	113.5	7.1	605	1	US-08-752-307B-8	Sequence 8, Appl	919	112.5	7.0	865	2	US-08-411-295F-248	Sequence 248, App
847	113.5	7.1	605	2	US-09-707-802-8	Sequence 8, Appl	920	112.5	7.0	899	2	US-08-467-602-364	Sequence 364, App
848	113.5	7.1	605	2	US-09-991-326-8	Sequence 8, Appl	921	112.5	7.0	899	2	US-08-411-295F-290	Sequence 290, App
849	113.5	7.1	640	2	US-09-949-016-7565	Sequence 7565, Ap	922	112.5	7.0	1209	2	US-08-411-295F-210	Sequence 210, App
850	113.5	7.1	643	5	PCT-US93-00031-19	Sequence 19, Appl	923	112	7.0	281	2	US-10-027-736A-67	Sequence 67, Appl
851	113.5	7.1	644	5	PCT-US93-00031-21	Sequence 21, Appl	924	112	7.0	283	2	US-10-198-053-624	Sequence 624, App
852	113.5	7.1	647	2	US-09-009-490A-91	Sequence 91, Appl	925	112	7.0	354	2	US-10-104-047-2965	Sequence 2965, Ap
853	113.5	7.1	647	2	US-08-482-073-5	Sequence 5, Appl	926	112	7.0	409	2	US-08-467-602-284	Sequence 284, App
854	113.5	7.1	647	2	US-09-982-262C-92	Sequence 92, Appl	927	112	7.0	409	2	US-08-411-295F-210	Sequence 210, App
855	113.5	7.1	647	5	PCT-US93-00031-11	Sequence 11, Appl	928	112	7.0	503	2	US-08-999-689A-6	Sequence 6, Appl
856	113.5	7.1	647	5	PCT-US93-00031-23	Sequence 23, Appl	929	112	7.0	503	2	US-09-944-807-4	Sequence 4, Appl
857	113.5	7.1	650	2	US-08-467-602-280	Sequence 280, App	930	112	7.0	524	2	US-09-270-767-44009	Sequence 44009, A
858	113.5	7.1	650	2	US-08-411-295F-206	Sequence 206, App	931	112	7.0	524	2	US-08-467-602-285	Sequence 285, App
859	113.5	7.1	729	1	US-08-070-165F-6	Sequence 6, Appl	932	112	7.0	626	2	US-08-411-295F-211	Sequence 211, App
860	113.5	7.1	729	1	US-08-885-418-6	Sequence 6, Appl	933	112	7.0	626	2	US-08-467-602-283	Sequence 283, App
861	113	7.0	352	2	US-09-999-833A-612	Sequence 612, App	934	112	7.0	673	2	US-08-411-295F-209	Sequence 209, App
862	113	7.0	352	2	US-10-020-445A-612	Sequence 612, App	935	112	7.0	879	3	US-10-162-335-90	Sequence 90, Appl
863	113	7.0	352	2	US-09-978-189-612	Sequence 612, App	936	111	6.9	96	2	US-09-513-999C-7124	Sequence 7124, Ap
864	113	7.0	352	2	US-10-017-085A-612	Sequence 612, App	937	111	6.9	375	2	US-08-467-602-242	Sequence 242, App
865	113	7.0	352	3	US-10-145-129A-612	Sequence 612, App	938	111	6.9	375	2	US-08-411-295F-168	Sequence 168, App
866	113	7.0	352	3	US-10-013-929A-612	Sequence 612, App	939	111	6.9	592	2	US-08-467-602-243	Sequence 243, App
867	113	7.0	352	3	US-10-013-917A-612	Sequence 612, App	940	111	6.9	592	2	US-08-411-295F-169	Sequence 169, App
868	113	7.0	489	2	US-09-667-135-30	Sequence 30, Appl	941	111	6.9	624	2	US-08-467-602-326	Sequence 326, App
869	113	7.0	626	2	US-09-949-016-6213	Sequence 6213, Ap	942	111	6.9	624	2	US-08-411-295F-252	Sequence 252, App
870	113	7.0	664	2	US-09-949-016-7850	Sequence 7850, Ap	943	111	6.9	639	2	US-08-467-602-241	Sequence 241, App
871	112.5	7.0	248	7	5169835-15	Patent No. 5169835	944	111	6.9	639	2	US-08-411-295F-167	Sequence 167, App
872	112.5	7.0	288	1	US-08-147-773-2	Sequence 2, Appl	945	111	6.9	658	2	US-08-467-602-368	Sequence 368, App
873	112.5	7.0	288	1	US-08-456-104-6	Sequence 6, Appl	946	111	6.9	658	2	US-08-411-295F-294	Sequence 294, App
874	112.5	7.0	288	1	US-08-101-624-23	Sequence 23, Appl	947	111	6.9	841	2	US-08-467-602-327	Sequence 327, App
875	112.5	7.0	288	2	US-08-751-767A-6	Sequence 6, Appl	948	111	6.9	841	2	US-08-411-295F-253	Sequence 253, App
876	112.5	7.0	288	2	US-08-153-262-2	Sequence 2, Appl	949	111	6.9	875	2	US-08-467-602-369	Sequence 369, App
877	112.5	7.0	288	2	US-08-479-744A-29	Sequence 29, Appl	950	111	6.9	875	2	US-08-411-295F-295	Sequence 295, App
878	112.5	7.0	288	2	US-08-280-757B-29	Sequence 29, Appl	951	111	6.9	888	2	US-08-467-602-325	Sequence 325, App
879	112.5	7.0	288	2	US-09-159-135-2	Sequence 2, Appl	952	111	6.9	888	2	US-08-411-295F-251	Sequence 251, App
880	112.5	7.0	288	2	US-08-205-697A-19	Sequence 19, Appl	953	111	6.9	922	2	US-08-467-602-367	Sequence 367, App
881	112.5	7.0	288	2	US-08-702-523-19	Sequence 19, Appl	954	111	6.9	922	2	US-08-411-295F-293	Sequence 293, App
882	112.5	7.0	288	2	US-09-450-798-2	Sequence 2, Appl	955	110.5	6.9	170	2	US-09-270-767-43106	Sequence 43106, A
883	112.5	7.0	288	2	US-08-403-253A-2	Sequence 2, Appl	956	110.5	6.9	512	2	US-08-999-689A-7	Sequence 7, Appl
884	112.5	7.0	288	2	US-09-651-200-13	Sequence 13, Appl	957	110	6.9	336	2	US-10-027-736A-65	Sequence 65, Appl
885	112.5	7.0	288	2	US-09-667-135-34	Sequence 34, Appl	958	110	6.9	357	2	US-10-027-736A-9	Sequence 9, Appl
886	112.5	7.0	288	2	US-08-435-818A-2	Sequence 2, Appl	959	110	6.9	422	2	US-08-753-007A-9	Sequence 9, Appl
887	112.5	7.0	288	2	US-09-425-762-29	Sequence 29, Appl	960	110	6.9	442	2	US-09-398-496-9	Sequence 9, Appl
888	112.5	7.0	288	2	US-09-837-867A-19	Sequence 19, Appl	961	110	6.9	1461	2	US-09-976-594-531	Sequence 531, App
889	112.5	7.0	288	2	US-09-910-174B-5	Sequence 5, Appl	962	110	6.9	1503	2	US-09-677-046A-6	Sequence 6, Appl
890	112.5	7.0	288	2	US-09-620-461-5	Sequence 5, Appl	963	109.5	6.8	316	2	US-09-999-833A-137	Sequence 137, App
891	112.5	7.0	288	2	US-08-453-386A-2	Sequence 2, Appl	964	109.5	6.8	316	2	US-10-020-445A-137	Sequence 137, App
892	112.5	7.0	288	2	US-09-206-132-6	Sequence 6, Appl	965	109.5	6.8	316	2	US-09-875-338-11	Sequence 11, Appl
893	112.5	7.0	288	2	US-09-425-516-29	Sequence 29, Appl	966	109.5	6.8	316	2	US-09-978-189-137	Sequence 137, App
894	112.5	7.0	288	2	US-09-350-202-2	Sequence 2, Appl	967	109.5	6.8	316	3	US-10-017-085A-137	Sequence 137, App
895	112.5	7.0	288	2	US-09-915-789A-15	Sequence 15, Appl	968	109.5	6.8	316	3	US-10-145-129A-137	Sequence 137, App
896	112.5	7.0	288	2	US-08-592-711-2	Sequence 2, Appl	969	109.5	6.8	316	3	US-10-013-929A-137	Sequence 137, App
897	112.5	7.0	288	2	US-09-349-915B-2	GENERAL INFORNA	970	109.5	6.8	316	3	US-10-013-917A-137	Sequence 137, App
898	112.5	7.0	288	3	US-09-565-316A-2	Sequence 2, Appl	971	109.5	6.8	350	2	US-09-651-200-25	Sequence 25, Appl
899	112.5	7.0	288	5	PCT-US95-02576-19	Sequence 19, Appl	972	109.5	6.8	350	2	US-09-910-174B-17	Sequence 17, Appl
900	112.5	7.0	352	2	US-08-467-602-239	Sequence 239, App	973	109.5	6.8	350	2	US-09-620-461-17	Sequence 17, Appl
901	112.5	7.0	352	2	US-08-411-295F-165	Sequence 165, App	974	109.5	6.8	373	2	US-09-823-038A-60	Sequence 60, Appl
902	112.5	7.0	569	2	US-08-467-602-237	Sequence 237, App	975	109.5	6.8	418	2	US-08-467-602-293	Sequence 293, App

976	109.5	6.8	418	2	US-08-411-295F-219	Sequence 219, App	1049	108.5	6.8	450	2	US-09-906-618-320	Sequence 320, App
977	109.5	6.8	466	2	US-10-012-231A-267	Sequence 267, App	1050	108.5	6.8	450	2	US-09-906-646-320	Sequence 320, App
978	109.5	6.8	466	2	US-10-015-389A-267	Sequence 267, App	1051	108.5	6.8	450	2	US-09-904-462-320	Sequence 320, App
979	109.5	6.8	466	2	US-10-006-768A-267	Sequence 267, App	1052	108.5	6.8	450	2	US-09-902-736A-320	Sequence 320, App
980	109.5	6.8	466	2	US-10-015-671A-267	Sequence 267, App	1053	108.5	6.8	450	2	US-09-902-722A-320	Sequence 320, App
981	109.5	6.8	466	2	US-10-015-393A-267	Sequence 267, App	1054	108.5	6.8	450	2	US-09-905-449-320	Sequence 320, App
982	109.5	6.8	466	2	US-10-011-833A-267	Sequence 267, App	1055	108.5	6.8	450	2	US-09-906-562B-320	Sequence 320, App
983	109.5	6.8	466	2	US-10-006-041A-267	Sequence 267, App	1056	108.5	6.8	450	2	US-09-906-679A-320	Sequence 320, App
984	109.5	6.8	466	2	US-10-012-064A-267	Sequence 267, App	1057	108.5	6.8	450	3	US-09-907-841-320	Sequence 320, App
985	109.5	6.8	466	2	US-10-015-392A-267	Sequence 267, App	1058	108.5	6.8	601	2	US-08-467-602-252	Sequence 252, App
986	109.5	6.8	466	3	US-10-011-795B-267	Sequence 267, App	1059	108.5	6.8	601	2	US-08-411-295F-178	Sequence 178, App
987	109.5	6.8	466	3	US-10-015-386A-267	Sequence 267, App	1060	108.5	6.8	615	2	US-08-467-602-288	Sequence 288, App
988	109.5	6.8	466	3	US-10-012-121A-267	Sequence 267, App	1061	108.5	6.8	615	2	US-08-411-295F-214	Sequence 214, App
989	109.5	6.8	466	3	US-10-012-121A-267	Sequence 267, App	1062	108.5	6.8	633	2	US-08-467-602-335	Sequence 335, App
990	109.5	6.8	466	3	US-10-006-485A-267	Sequence 267, App	1063	108.5	6.8	633	2	US-08-411-295F-261	Sequence 261, App
991	109.5	6.8	466	3	US-10-012-752A-267	Sequence 267, App	1064	108.5	6.8	637	1	US-07-847-743B-28	Sequence 28, Appl
992	109.5	6.8	466	3	US-10-017-253A-267	Sequence 267, App	1065	108.5	6.8	637	1	US-08-456-201-28	Sequence 28, Appl
993	109.5	6.8	466	3	US-10-015-519A-267	Sequence 267, App	1066	108.5	6.8	637	1	US-08-456-241-28	Sequence 28, Appl
994	109.5	6.8	466	3	US-10-017-715A-267	Sequence 267, App	1067	108.5	6.8	637	5	PCT-US92-04295A-28	Sequence 253, App
995	109.5	6.8	466	3	US-10-007-236A-267	Sequence 267, App	1068	108.5	6.8	648	2	US-08-467-602-253	Sequence 253, App
996	109.5	6.8	529	2	US-09-383-586-31	Sequence 31, Appl	1069	108.5	6.8	648	2	US-08-411-295F-179	Sequence 179, App
997	109.5	6.8	529	2	US-09-823-038A-31	Sequence 31, Appl	1070	108.5	6.8	662	2	US-08-467-602-289	Sequence 289, App
998	109.5	6.8	534	2	US-09-651-200-6	Sequence 6, Appl	1071	108.5	6.8	662	2	US-08-411-295F-215	Sequence 215, App
999	109.5	6.8	534	2	US-09-651-200-24	Sequence 24, Appl	1072	108.5	6.8	667	2	US-08-467-602-377	Sequence 377, App
1000	109.5	6.8	534	2	US-09-875-338-7	Sequence 7, Appl	1073	108.5	6.8	667	2	US-08-411-295F-303	Sequence 303, App
1001	109.5	6.8	635	2	US-08-467-602-294	Sequence 294, App	1074	108.5	6.8	850	2	US-08-467-602-336	Sequence 336, App
1002	109.5	6.8	635	2	US-08-411-295F-220	Sequence 220, App	1075	108.5	6.8	850	2	US-08-411-295F-262	Sequence 262, App
1003	109.5	6.8	682	2	US-08-467-602-295	Sequence 295, App	1076	108.5	6.8	884	2	US-08-467-602-378	Sequence 378, App
1004	109.5	6.8	682	2	US-08-411-295F-221	Sequence 221, App	1077	108.5	6.8	884	2	US-08-411-295F-304	Sequence 304, App
1005	109	6.8	79	2	US-09-621-976-4730	Sequence 4730, Ap	1078	108.5	6.8	897	2	US-08-467-602-337	Sequence 337, App
1006	109	6.8	118	2	US-10-094-749-3260	Sequence 3260, Ap	1079	108.5	6.8	897	2	US-08-411-295F-263	Sequence 263, App
1007	109	6.8	286	2	US-09-270-767-44618	Sequence 44618, A	1080	108.5	6.8	924	1	US-08-481-130-28	Sequence 28, Appl
1008	109	6.8	395	2	US-08-467-602-290	Sequence 290, App	1081	108.5	6.8	924	1	US-08-656-984A-28	Sequence 28, Appl
1009	109	6.8	395	2	US-08-411-295F-216	Sequence 216, App	1082	108.5	6.8	924	1	US-08-485-604-28	Sequence 28, Appl
1010	109	6.8	405	2	US-08-755-235-4	Sequence 4, Appl	1083	108.5	6.8	924	1	US-08-487-595-28	Sequence 28, Appl
1011	109	6.8	612	2	US-08-467-602-291	Sequence 291, App	1084	108.5	6.8	931	2	US-08-467-602-379	Sequence 379, App
1012	109	6.8	612	2	US-08-411-295F-217	Sequence 217, App	1085	108.5	6.8	931	2	US-08-411-295F-305	Sequence 305, App
1013	109	6.8	619	2	US-10-104-047-2048	Sequence 2048, Ap	1086	108	6.7	939	2	US-09-719-243-2	Sequence 2, Appl
1014	109	6.8	630	1	US-08-752-307B-14	Sequence 14, Appl	1087	108	6.7	361	2	US-08-467-602-248	Sequence 248, App
1015	109	6.8	630	2	US-09-707-802-14	Sequence 14, Appl	1088	108	6.7	361	2	US-08-411-295F-174	Sequence 174, App
1016	109	6.8	630	2	US-09-991-326-14	Sequence 14, Appl	1089	108	6.7	456	2	US-08-470-335-246	Sequence 246, App
1017	109	6.8	659	2	US-08-467-602-292	Sequence 292, App	1090	108	6.7	456	2	US-08-467-602-303	Sequence 303, App
1018	109	6.8	659	2	US-08-411-295F-218	Sequence 218, App	1091	108	6.7	456	2	US-08-411-295F-229	Sequence 229, App
1019	109	6.8	816	2	US-09-949-016-10904	Sequence 10904, A	1092	108	6.7	459	2	US-08-470-335-239	Sequence 239, App
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1021	109	6.8	917	1	US-08-245-295-2	Sequence 2, Appl	1094	108	6.7	459	2	US-08-411-295F-225	Sequence 225, App
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1023	109	6.8	917	1	US-08-656-984A-2	Sequence 2, Appl	1096	108	6.7	479	2	US-08-411-295F-233	Sequence 233, App
1024	109	6.8	917	1	US-08-485-604-2	Sequence 2, Appl	1097	108	6.7	490	2	US-08-467-602-345	Sequence 345, App
1025	109	6.8	917	1	US-08-487-595-2	Sequence 2, Appl	1098	108	6.7	490	2	US-08-411-295F-271	Sequence 271, App
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1027	108.5	6.8	340	2	US-09-651-200-2	Sequence 2, Appl	1100	108	6.7	493	2	US-08-411-295F-267	Sequence 267, App
1028	108.5	6.8	384	2	US-08-467-602-251	Sequence 251, App	1101	108	6.7	513	2	US-08-467-602-349	Sequence 349, App
1029	108.5	6.8	384	2	US-08-411-295F-177	Sequence 177, App	1102	108	6.7	513	2	US-08-411-295F-275	Sequence 275, App
1030	108.5	6.8	398	2	US-08-467-602-287	Sequence 287, App	1103	108	6.7	578	2	US-08-467-602-249	Sequence 249, App
1031	108.5	6.8	398	2	US-08-411-295F-213	Sequence 213, App	1104	108	6.7	578	2	US-08-411-295F-175	Sequence 175, App
1032	108.5	6.8	404	2	US-09-638-649-3	Sequence 3, Appl	1105	108	6.7	610	2	US-08-470-335-236	Sequence 236, App
1033	108.5	6.8	404	2	US-09-949-016-11025	Sequence 11025, A	1106	108	6.7	610	2	US-08-467-602-332	Sequence 332, App
1034	108.5	6.8	404	2	US-09-638-648-3	Sequence 3, Appl	1107	108	6.7	610	2	US-08-411-295F-258	Sequence 258, App
1035	108.5	6.8	404	2	US-09-799-152-1	Sequence 1, Appl	1108	108	6.7	625	2	US-08-467-602-250	Sequence 250, App
1036	108.5	6.8	420	1	US-07-847-743B-29	Sequence 29, Appl	1109	108	6.7	625	2	US-08-411-295F-176	Sequence 176, App
1037	108.5	6.8	420	1	US-08-456-201-29	Sequence 29, Appl	1110	108	6.7	635	2	US-08-470-335-247	Sequence 302, App
1038	108.5	6.8	420	1	US-08-456-241-29	Sequence 29, Appl	1111	108	6.7	635	2	US-08-467-602-302	Sequence 288, App
1039	108.5	6.8	420	5	PCT-US92-04295A-29	Sequence 29, Appl	1112	108	6.7	635	2	US-08-411-295F-228	Sequence 228, App
1040	108.5	6.8	441	2	US-09-651-200-4	Sequence 4, Appl	1113	108	6.7	638	2	US-08-470-335-240	Sequence 240, App
1041	108.5	6.8	450	2	US-09-907-794A-320	Sequence 320, App	1114	108	6.7	638	2	US-08-467-602-297	Sequence 297, App
1042	108.5	6.8	450	2	US-09-905-125A-320	Sequence 320, App	1115	108	6.7	638	2	US-08-411-295F-223	Sequence 223, App
1043	108.5	6.8	450	2	US-09-902-775A-320	Sequence 320, App	1116	108	6.7	644	2	US-08-470-335-250	Sequence 250, App
1044	108.5	6.8	450	2	US-09-906-700-320	Sequence 320, App	1117	108	6.7	644	2	US-08-467-602-311	Sequence 311, App
1045	108.5	6.8	450	2	US-09-903-603A-320	Sequence 320, App	1118	108	6.7	644	2	US-08-467-602-374	Sequence 374, App
1046	108.5	6.8	450	2	US-09-904-920A-320	Sequence 320, App	1119	108	6.7	644	2	US-08-411-295F-237	Sequence 237, App
1047	108.5	6.8	450	2	US-09-909-064-320	Sequence 320, App	1120	108	6.7	644	2	US-08-411-295F-300	Sequence 300, App
1048	108.5	6.8	450	2	US-09-905-381A-320	Sequence 320, App	1121	108	6.7	647	2	US-08-470-335-243	Sequence 243, App

1122	108	6.7	647	2	US-08-467-602-308	Sequence 308, App	1195	108	6.7	933	2	US-08-411-295F-269	Sequence 269, App
1123	108	6.7	647	2	US-08-411-295F-234	Sequence 234, App	1196	108	6.7	936	2	US-08-467-602-338	Sequence 338, App
1124	108	6.7	658	2	US-08-467-602-305	Sequence 305, App	1197	108	6.7	936	2	US-08-411-295F-264	Sequence 264, App
1125	108	6.7	658	2	US-08-411-295F-231	Sequence 231, App	1198	108	6.7	942	2	US-08-467-602-355	Sequence 355, App
1126	108	6.7	667	2	US-08-467-602-314	Sequence 314, App	1199	108	6.7	942	2	US-08-411-295F-281	Sequence 281, App
1127	108	6.7	667	2	US-08-411-295F-240	Sequence 240, App	1200	108	6.7	945	2	US-08-467-602-352	Sequence 352, App
1128	108	6.7	669	2	US-08-467-602-344	Sequence 344, App	1201	108	6.7	945	2	US-08-411-295F-278	Sequence 278, App
1129	108	6.7	669	2	US-08-411-295F-270	Sequence 270, App	1202	108	6.7	956	2	US-08-467-602-346	Sequence 346, App
1130	108	6.7	672	2	US-08-467-602-339	Sequence 339, App	1203	108	6.7	956	2	US-08-411-295F-272	Sequence 272, App
1131	108	6.7	672	2	US-08-411-295F-265	Sequence 265, App	1204	108	6.7	965	2	US-08-467-602-358	Sequence 358, App
1132	108	6.7	678	2	US-08-467-602-353	Sequence 353, App	1205	108	6.7	965	2	US-08-411-295F-284	Sequence 284, App
1133	108	6.7	678	2	US-08-411-295F-279	Sequence 279, App	1206	107.5	6.7	262	2	US-10-104-047-3119	Sequence 3119, App
1134	108	6.7	681	2	US-08-467-602-350	Sequence 350, App	1207	107.5	6.7	316	2	US-09-910-174B-24	Sequence 24, App
1135	108	6.7	681	2	US-08-411-295F-276	Sequence 276, App	1208	107.5	6.7	316	2	US-09-620-461-24	Sequence 24, App
1136	108	6.7	692	2	US-08-467-602-347	Sequence 347, App	1209	107.5	6.7	316	2	US-09-915-789A-1	Sequence 1, App
1137	108	6.7	692	2	US-08-411-295F-273	Sequence 273, App	1210	107.5	6.7	316	2	US-09-875-338-13	Sequence 13, App
1138	108	6.7	701	2	US-08-467-602-356	Sequence 356, App	1211	107.5	6.7	358	2	US-09-719-243-3	Sequence 3, App
1139	108	6.7	701	2	US-08-411-295F-282	Sequence 282, App	1212	107.5	6.7	364	2	US-08-467-602-245	Sequence 245, App
1140	108	6.7	827	2	US-08-470-335-233	Sequence 233, App	1213	107.5	6.7	364	2	US-08-411-295F-171	Sequence 171, App
1141	108	6.7	827	2	US-08-467-602-337	Sequence 337, App	1214	107.5	6.7	420	2	US-08-467-602-260	Sequence 260, App
1142	108	6.7	827	2	US-08-411-295F-259	Sequence 259, App	1215	107.5	6.7	420	2	US-08-411-295F-186	Sequence 186, App
1143	108	6.7	852	2	US-08-470-335-248	Sequence 248, App	1216	107.5	6.7	581	2	US-08-467-602-246	Sequence 246, App
1144	108	6.7	852	2	US-08-467-602-300	Sequence 300, App	1217	107.5	6.7	581	2	US-08-411-295F-172	Sequence 172, App
1145	108	6.7	852	2	US-08-411-295F-226	Sequence 226, App	1218	107.5	6.7	613	2	US-08-470-335-230	Sequence 230, App
1146	108	6.7	855	2	US-08-470-335-241	Sequence 241, App	1219	107.5	6.7	613	2	US-08-467-602-329	Sequence 329, App
1147	108	6.7	855	2	US-08-467-602-298	Sequence 298, App	1220	107.5	6.7	613	2	US-08-411-295F-255	Sequence 255, App
1148	108	6.7	855	2	US-08-411-295F-224	Sequence 224, App	1221	107.5	6.7	628	2	US-08-467-602-247	Sequence 247, App
1149	108	6.7	861	2	US-08-470-335-251	Sequence 251, App	1222	107.5	6.7	628	2	US-08-411-295F-173	Sequence 173, App
1150	108	6.7	861	2	US-08-467-602-312	Sequence 312, App	1223	107.5	6.7	637	2	US-08-467-602-258	Sequence 258, App
1151	108	6.7	861	2	US-08-467-602-375	Sequence 375, App	1224	107.5	6.7	637	2	US-08-411-295F-184	Sequence 184, App
1152	108	6.7	861	2	US-08-411-295F-238	Sequence 238, App	1225	107.5	6.7	647	2	US-08-467-602-371	Sequence 371, App
1153	108	6.7	861	2	US-08-411-295F-301	Sequence 301, App	1226	107.5	6.7	647	2	US-08-411-295F-297	Sequence 297, App
1154	108	6.7	864	2	US-08-470-335-244	Sequence 244, App	1227	107.5	6.7	684	2	US-08-467-602-259	Sequence 259, App
1155	108	6.7	864	2	US-08-467-602-309	Sequence 309, App	1228	107.5	6.7	684	2	US-08-411-295F-185	Sequence 185, App
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1158	108	6.7	874	2	US-08-467-602-334	Sequence 334, App	1231	107.5	6.7	733	1	US-08-441-944A-6	Sequence 6, App
1159	108	6.7	874	2	US-08-411-295F-260	Sequence 260, App	1232	107.5	6.7	733	2	US-08-439-992A-4	Sequence 4, App
1160	108	6.7	875	2	US-08-467-602-306	Sequence 306, App	1233	107.5	6.7	733	2	US-09-620-561-4	Sequence 4, App
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1170	108	6.7	898	2	US-08-467-602-351	Sequence 351, App	1243	107.5	6.7	911	2	US-08-411-295F-299	Sequence 299, App
1171	108	6.7	898	2	US-08-411-295F-277	Sequence 277, App	1244	107	6.7	100	2	US-09-621-976-3911	Sequence 3911, App
1172	108	6.7	899	2	US-08-470-335-249	Sequence 249, App	1245	107	6.7	110	2	US-09-513-999C-7253	Sequence 7253, App
1173	108	6.7	899	2	US-08-467-602-301	Sequence 301, App	1246	107	6.7	389	2	US-08-467-602-276	Sequence 276, App
1174	108	6.7	899	2	US-08-411-295F-227	Sequence 227, App	1247	107	6.7	389	2	US-08-411-295F-202	Sequence 202, App
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1183	108	6.7	909	2	US-08-467-602-348	Sequence 348, App	1256	107	6.7	653	2	US-08-467-602-275	Sequence 275, App
1184	108	6.7	909	2	US-08-411-295F-274	Sequence 274, App	1257	107	6.7	653	2	US-08-411-295F-201	Sequence 201, App
1185	108	6.7	911	2	US-08-470-335-245	Sequence 245, App	1258	107	6.7	1298	2	US-09-499-468-38	Sequence 38, App
1186	108	6.7	911	2	US-08-467-602-310	Sequence 310, App	1259	106.5	6.6	316	2	US-09-451-291-10	Sequence 10, App
1187	108	6.7	911	2	US-08-411-295F-236	Sequence 236, App	1260	106.5	6.6	316	2	US-09-915-789A-3	Sequence 3, App
1188	108	6.7	918	2	US-08-467-602-357	Sequence 357, App	1261	106.5	6.6	386	2	US-08-467-602-218	Sequence 218, App
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1191	108	6.7	922	2	US-08-411-295F-230	Sequence 230, App	1264	106.5	6.6	603	2	US-08-411-295F-142	Sequence 142, App
1192	108	6.7	931	2	US-08-467-602-316	Sequence 316, App	1265	106.5	6.6	650	2	US-08-467-602-217	Sequence 217, App
1193	108	6.7	931	2	US-08-411-295F-242	Sequence 242, App	1266	106.5	6.6	650	2	US-08-411-295F-143	Sequence 143, App
1194	108	6.7	933	2	US-08-467-602-343	Sequence 343, App	1267	106.5	6.6	731	1	US-08-070-165F-10	Sequence 10, App

1268	106.5	6.6	731	1	US-08-885-418-10	Sequence 10, Appl	1341	104.5	6.5	259	2	US-10-104-047-2303	Sequence 2303, Ap
1269	106.5	6.6	879	1	US-08-554-612C-1	Sequence 1, Appl	1342	104.5	6.5	313	2	US-09-610-118-44	Sequence 44, Appl
1270	106	6.6	355	2	US-08-467-602-234	Sequence 234, Appl	1343	104.5	6.5	518	2	US-09-919-172-20	Sequence 20, Appl
1271	106	6.6	355	2	US-08-411-295F-160	Sequence 160, Appl	1344	104.5	6.5	645	2	US-08-753-007A-10	Sequence 10, Appl
1272	106	6.6	443	2	US-08-467-602-263	Sequence 263, Appl	1345	104.5	6.5	645	2	US-09-398-496-10	Sequence 10, Appl
1273	106	6.6	443	2	US-08-411-295F-189	Sequence 189, Appl	1346	104.5	6.5	777	1	US-08-874-678-3	Sequence 3, Appl
1274	106	6.6	572	2	US-08-467-602-235	Sequence 235, Appl	1347	104.5	6.5	777	2	US-08-643-839-3	Sequence 3, Appl
1275	106	6.6	572	2	US-08-411-295F-161	Sequence 161, Appl	1348	104.5	6.5	777	2	US-09-348-886-3	Sequence 3, Appl
1276	106	6.6	604	2	US-08-470-335-227	Sequence 227, Appl	1349	104.5	6.5	777	2	US-10-105-901A-3	Sequence 3, Appl
1277	106	6.6	604	2	US-08-467-602-318	Sequence 318, Appl	1350	104	6.5	236	2	US-09-015-734-7	Sequence 7, Appl
1278	106	6.6	604	2	US-08-411-295F-244	Sequence 244, Appl	1351	104	6.5	236	2	US-09-515-311-7	Sequence 7, Appl
1279	106	6.6	619	2	US-08-467-602-233	Sequence 233, Appl	1352	104	6.5	236	2	US-10-434-817-7	Sequence 7, Appl
1280	106	6.6	619	2	US-08-411-295F-159	Sequence 159, Appl	1353	104	6.5	255	2	US-09-015-734-2	Sequence 2, Appl
1281	106	6.6	638	2	US-08-467-602-360	Sequence 360, Appl	1354	104	6.5	255	2	US-09-515-311-2	Sequence 2, Appl
1282	106	6.6	638	2	US-08-411-295F-286	Sequence 286, Appl	1355	104	6.5	255	2	US-10-434-817-2	Sequence 2, Appl
1283	106	6.6	660	2	US-08-467-602-264	Sequence 264, Appl	1356	104	6.5	491	2	US-10-094-749-2931	Sequence 2931, Ap
1284	106	6.6	660	2	US-08-411-295F-190	Sequence 190, Appl	1357	104	6.5	802	2	US-09-173-151A-33	Sequence 33, Appl
1285	106	6.6	707	2	US-08-467-602-262	Sequence 262, Appl	1358	103.5	6.4	313	2	US-09-610-118-46	Sequence 46, Appl
1286	106	6.6	707	2	US-08-467-602-361	Sequence 361, Appl	1359	103.5	6.4	388	1	US-08-429-742-4	Sequence 4, Appl
1287	106	6.6	821	2	US-08-411-295F-188	Sequence 188, Appl	1360	103.5	6.4	452	2	US-08-467-602-272	Sequence 272, App
1288	106	6.6	821	2	US-08-467-602-319	Sequence 319, Appl	1361	103.5	6.4	452	2	US-08-411-295F-198	Sequence 198, App
1289	106	6.6	821	2	US-08-411-295F-245	Sequence 245, Appl	1362	103.5	6.4	669	2	US-08-467-602-273	Sequence 273, App
1290	106	6.6	855	2	US-08-467-602-361	Sequence 361, Appl	1363	103.5	6.4	669	2	US-08-411-295F-199	Sequence 199, App
1291	106	6.6	855	2	US-08-411-295F-287	Sequence 287, Appl	1364	103.5	6.4	716	2	US-08-467-602-274	Sequence 274, App
1292	106	6.6	868	2	US-08-470-335-229	Sequence 229, Appl	1365	103.5	6.4	716	2	US-08-411-295F-200	Sequence 200, App
1293	106	6.6	868	2	US-08-467-602-317	Sequence 317, Appl	1366	103.5	6.4	731	1	US-07-921-807B-5	Sequence 5, Appl
1294	106	6.6	868	2	US-08-411-295F-243	Sequence 243, Appl	1367	103.5	6.4	731	1	US-08-441-944A-5	Sequence 5, Appl
1295	106	6.6	902	2	US-08-467-602-359	Sequence 359, Appl	1368	103.5	6.4	731	2	US-08-439-992A-3	Sequence 3, Appl
1296	106	6.6	902	2	US-08-411-295F-285	Sequence 285, Appl	1369	103.5	6.4	731	2	US-09-620-561-3	Sequence 3, Appl
1297	105.5	6.6	235	2	US-09-646-561-12	Sequence 12, Appl	1370	103	6.4	58	2	US-09-621-976-5931	Sequence 5931, Ap
1298	105.5	6.6	267	2	US-09-345-468-19	Sequence 19, Appl	1371	103	6.4	58	2	US-09-621-976-5963	Sequence 5963, Ap
1299	105.5	6.6	267	2	US-09-414-453A-19	Sequence 19, Appl	1372	103	6.4	58	2	US-09-621-976-6579	Sequence 6579, Ap
1300	105.5	6.6	267	2	US-09-610-118-19	Sequence 19, Appl	1373	103	6.4	71	2	US-09-621-976-5970	Sequence 5970, Ap
1301	105.5	6.6	267	2	US-09-345-468-18	Sequence 18, Appl	1374	103	6.4	71	2	US-09-621-976-6815	Sequence 6815, Ap
1302	105.5	6.6	292	2	US-09-414-453A-18	Sequence 18, Appl	1375	103	6.4	71	2	US-09-621-976-6875	Sequence 6875, Ap
1303	105.5	6.6	292	2	US-09-610-118-18	Sequence 18, Appl	1376	103	6.4	133	2	US-10-104-047-3128	Sequence 3128, Ap
1304	105.5	6.6	313	2	US-09-345-468-16	Sequence 16, Appl	1377	103	6.4	208	2	US-09-460-384-36	Sequence 36, Ap
1305	105.5	6.6	313	2	US-09-414-453A-16	Sequence 16, Appl	1378	103	6.4	216	2	US-09-666-267B-8	Sequence 8, Appl
1306	105.5	6.6	313	2	US-09-610-118-16	Sequence 16, Appl	1379	103	6.4	216	2	US-09-454-651B-23	Sequence 23, Appl
1307	105.5	6.6	313	2	US-09-610-118-48	Sequence 48, Appl	1380	103	6.4	226	2	US-09-915-789A-21	Sequence 21, Appl
1308	105.5	6.6	498	2	US-09-354-151-2	Sequence 2, Appl	1381	103	6.4	240	1	US-08-471-570-12	Sequence 12, Appl
1309	105.5	6.6	624	1	US-08-642-406A-22	Sequence 22, Appl	1382	103	6.4	428	2	US-09-949-016-6625	Sequence 6625, Ap
1310	105.5	6.6	624	2	US-09-199-534-22	Sequence 22, Appl	1383	103	6.4	429	2	US-08-467-602-269	Sequence 269, App
1311	105.5	6.6	624	2	US-09-199-534-22	Sequence 22, Appl	1384	103	6.4	429	2	US-08-411-295F-195	Sequence 195, App
1312	105.5	6.6	624	2	US-09-491-322-22	Sequence 22, Appl	1385	103	6.4	433	2	US-09-949-016-8521	Sequence 8521, Ap
1313	105.5	6.6	624	3	US-09-200-657-22	Sequence 22, Appl	1386	103	6.4	473	2	US-09-171-945-131	Sequence 131, App
1314	105.5	6.6	645	1	US-07-847-743B-27	Sequence 27, Appl	1387	103	6.4	473	2	US-09-910-059-131	Sequence 131, App
1315	105.5	6.6	645	1	US-08-456-201-27	Sequence 27, Appl	1388	103	6.4	646	2	US-08-411-295F-196	Sequence 196, App
1316	105.5	6.6	645	1	US-08-428-926-4	Sequence 4, Appl	1389	103	6.4	646	2	US-08-467-602-271	Sequence 271, App
1317	105.5	6.6	645	1	US-08-428-927-4	Sequence 4, Appl	1390	103	6.4	693	2	US-08-411-295F-197	Sequence 197, App
1318	105.5	6.6	645	1	US-08-428-298-4	Sequence 4, Appl	1391	103	6.4	693	2	US-09-579-692B-8	Sequence 8, Appl
1319	105.5	6.6	645	1	US-08-339-517-4	Sequence 4, Appl	1392	103	6.4	1140	2	US-09-489-039A-13452	Sequence 13452, A
1320	105.5	6.6	645	1	US-08-456-241-27	Sequence 27, Appl	1393	102.5	6.4	257	2	US-09-245-764-7	Sequence 7, Appl
1321	105.5	6.6	645	2	US-09-020-880-93	Sequence 93, Appl	1394	102.5	6.4	261	2	US-08-411-295F-4	Sequence 4, Appl
1322	105.5	6.6	645	2	US-09-101-544-93	Sequence 93, Appl	1395	102.5	6.4	263	2	US-08-411-295F-156	Sequence 156, App
1323	105.5	6.6	645	2	US-09-097-681-3	Sequence 3, Appl	1396	102.5	6.4	418	2	US-08-467-602-230	Sequence 230, App
1324	105.5	6.6	645	5	PCT-US92-04295A-27	Sequence 27, Appl	1397	102.5	6.4	418	2	US-08-411-295F-192	Sequence 192, App
1325	105.5	6.6	732	1	US-07-847-743B-9	Sequence 9, Appl	1398	102.5	6.4	432	2	US-08-467-602-266	Sequence 266, App
1326	105.5	6.6	732	1	US-08-456-201-9	Sequence 9, Appl	1399	102.5	6.4	432	2	US-08-411-295F-192	Sequence 192, App
1327	105.5	6.6	732	1	US-08-456-241-9	Sequence 9, Appl	1400	102.5	6.4	584	2	US-09-910-174B-16	Sequence 16, Appl
1328	105.5	6.6	732	5	PCT-US92-04295A-9	Sequence 9, Appl	1401	102.5	6.4	584	2	US-09-620-461-16	Sequence 16, Appl
1329	105.5	6.6	732	2	US-08-434-000A-2	Sequence 2, Appl	1402	102.5	6.4	610	1	US-08-724-394A-5	Sequence 5, Appl
1330	105.5	6.6	773	2	US-09-312-157-2	Sequence 2, Appl	1403	102.5	6.4	635	2	US-08-467-602-231	Sequence 231, App
1331	105.5	6.6	773	2	US-09-717-888-2	Sequence 2, Appl	1404	102.5	6.4	635	2	US-08-411-295F-157	Sequence 157, App
1332	105.5	6.6	773	2	US-09-818-247-6	Sequence 6, Appl	1405	102.5	6.4	649	2	US-08-467-602-267	Sequence 267, App
1333	105	6.6	144	7	5169835-8	Patent No. 5169835	1406	102.5	6.4	649	2	US-08-411-295F-193	Sequence 193, App
1334	105	6.5	374	2	US-10-027-736A-10	Sequence 10, Appl	1407	102.5	6.4	658	2	US-09-173-151A-35	Sequence 35, Appl
1335	105	6.5	409	2	US-08-467-602-221	Sequence 221, App	1408	102.5	6.4	682	2	US-08-467-602-232	Sequence 232, App
1336	105	6.5	409	2	US-08-411-295F-147	Sequence 147, App	1409	102.5	6.4	682	2	US-08-411-295F-158	Sequence 158, App
1337	105	6.5	626	2	US-08-467-602-222	Sequence 222, App	1410	102.5	6.4	696	2	US-08-467-602-268	Sequence 268, App
1338	105	6.5	626	2	US-08-411-295F-148	Sequence 148, App	1411	102.5	6.4	696	2	US-08-411-295F-194	Sequence 194, App
1339	105	6.5	673	2	US-08-467-602-220	Sequence 220, App	1412	102.5	6.4	696	3	US-09-876-790-4	Sequence 4, Appl
1340	105	6.5	673	2	US-08-411-295F-146	Sequence 146, App	1413	102	6.4	63	2	US-09-621-976-6056	Sequence 6056, Ap

Db 241 IAAVVVVALVISVCGLGVCYQAKRGYFSKTSFQKSNSSSKATTMSENVQWLTVPVIALW 300
QY 301 KAAAGSGRGQEF 312
Db 301 KAAAGSGRGQEF 312

RESULT 2

US-09-907-794A-64
; Sequence 64, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-794A-64

Query Match 100.0%; Score 1605; DB 2; Length 312;
Best Local Similarity 100.0%; Pred. No. 1e-148;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARRSRRLRLRLRLRLRYLVVALGYHKAYGFSAPKDDQVVTAVYQEAAILACKTPKKTVSSR 60
Db 1 MARRSRRLRLRLRLRLRYLVVALGYHKAYGFSAPKDDQVVTAVYQEAAILACKTPKKTVSSR 60
QY 61 LEWKKLGRSVFVYQOTLQGDPKNRAEMIDFNIRIKNVTRSDAGKYRCVVSAPSEQQN 120
Db 61 LEWKKLGRSVFVYQOTLQGDPKNRAEMIDFNIRIKNVTRSDAGKYRCVVSAPSEQQN 120
QY 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVLRCDKEGNPAPEYTFWKDGIRLLENPR 180
Db 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVLRCDKEGNPAPEYTFWKDGIRLLENPR 180
QY 181 LGSQSTNSYTTWNTKGTGLQFNTVSKLDGCEYSCARNVGYRRCPCGRMQVDDNLISGI 240
Db 181 LGSQSTNSYTTWNTKGTGLQFNTVSKLDGCEYSCARNVGYRRCPCGRMQVDDNLISGI 240
QY 241 IAAVVVVALVISVCGLGVCYQAKRGYFSKTSFQKSNSSSKATTMSENVQWLTVPVIALW 300
Db 241 IAAVVVVALVISVCGLGVCYQAKRGYFSKTSFQKSNSSSKATTMSENVQWLTVPVIALW 300
QY 301 KAAAGSGRGQEF 312
Db 301 KAAAGSGRGQEF 312

RESULT 3

US-09-905-125A-64
; Sequence 64, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14

US-09-902-775A-64

Query Match 100.0%; Score 1605; DB 2; Length 312;
Best Local Similarity 100.0%; Pred. No. 1e-148;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARRSRHRLLLRLYLVALGYHAYGFSAPKQDQVTVAVEYQBAAILACKTPKKTVSSR 60
Db |||||
QY 1 MARRSRHRLLLRLYLVALGYHAYGFSAPKQDQVTVAVEYQBAAILACKTPKKTVSSR 60
Db |||||
QY 61 LEWKLGSRVSFVYQOTLQDGFKNRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEQON 120
Db 61 LEWKLGSRVSFVYQOTLQDGFKNRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEQON 120
QY 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVLRQDKEGNPAPEYTFWKDGIRLLENPR 180
Db 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVLRQDKEGNPAPEYTFWKDGIRLLENPR 180
QY 181 LGSQSTNSSTYMTNTKGTLOFNTVSKLDTGEYSCBARNVGYRRCPGKRMQVDDDLN1SGI 240
Db 181 LGSQSTNSSTYMTNTKGTLOFNTVSKLDTGEYSCBARNVGYRRCPGKRMQVDDDLN1SGI 240
QY 241 IAAVVVVALVISVCGLGVCYQAQRKGYSKETSFKQSNSSSKATTMSENVQWLTPVIPALW 300
Db 241 IAAVVVVALVISVCGLGVCYQAQRKGYSKETSFKQSNSSSKATTMSENVQWLTPVIPALW 300
QY 301 KAAAGSGRQGEF 312
Db 301 KAAAGSGRQGEF 312

RESULT 5

US-09-906-700-64
; Sequence 64, Application US/09906700
; Patent No. 6723535
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,700
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222

; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-700-64

Query Match 100.0%; Score 1605; DB 2; Length 312;
Best Local Similarity 100.0%; Pred. No. 1e-148;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARRSRHRLLLRLYLVALGYHAYGFSAPKQDQVTVAVEYQBAAILACKTPKKTVSSR 60
Db |||||
QY 1 MARRSRHRLLLRLYLVALGYHAYGFSAPKQDQVTVAVEYQBAAILACKTPKKTVSSR 60
Db |||||
QY 61 LEWKLGSRVSFVYQOTLQDGFKNRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEQON 120
Db 61 LEWKLGSRVSFVYQOTLQDGFKNRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEQON 120
QY 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVLRQDKEGNPAPEYTFWKDGIRLLENPR 180
Db 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVLRQDKEGNPAPEYTFWKDGIRLLENPR 180
QY 181 LGSQSTNSSTYMTNTKGTLOFNTVSKLDTGEYSCBARNVGYRRCPGKRMQVDDDLN1SGI 240
Db 181 LGSQSTNSSTYMTNTKGTLOFNTVSKLDTGEYSCBARNVGYRRCPGKRMQVDDDLN1SGI 240
QY 241 IAAVVVVALVISVCGLGVCYQAQRKGYSKETSFKQSNSSSKATTMSENVQWLTPVIPALW 300
Db 241 IAAVVVVALVISVCGLGVCYQAQRKGYSKETSFKQSNSSSKATTMSENVQWLTPVIPALW 300
QY 301 KAAAGSGRQGEF 312
Db 301 KAAAGSGRQGEF 312

RESULT 6

US-09-903-603A-64
; Sequence 64, Application US/09903603A
; Patent No. 6767995
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: GNE.1618P2C12
CURRENT APPLICATION NUMBER: US/09/903,603A
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 64
LENGTH: 312
TYPE: PRT
ORGANISM: Homo sapiens
US-09-903-603A-64

Query Match 100.0%; Score 1605; DB 2; Length 312;
Best Local Similarity 100.0%; Pred. No. 1e-148;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARRSRRLLLRLRLVVALGVHKGAFSAPKDDQVWTAVEYQEAAILACKTPKKTVSSR 60
DB 1 MARRSRRLLLRLRLVVALGVHKGAFSAPKDDQVWTAVEYQEAAILACKTPKKTVSSR 60

QY 61 LEWKKLGRSVSFVYQOTLOGDFKRAEMIDFNIRIKNVTRSDAGKYCEVSAPSEQGN 120
DB 61 LEWKKLGRSVSFVYQOTLOGDFKRAEMIDFNIRIKNVTRSDAGKYCEVSAPSEQGN 120
QY 121 LEEDTVTLVLVAPVPSCVPSALSGTGVVLELRCQDKEGNPAPEYTWFKDGIRLLENPR 180
DB 121 LEEDTVTLVLVAPVPSCVPSALSGTGVVLELRCQDKEGNPAPEYTWFKDGIRLLENPR 180
QY 181 LGSQSTNSSYTMNTKTGTLOFNTVSKLDTGYSCEARNVGYRRCPCGRMVDLNLISGI 240
DB 181 LGSQSTNSSYTMNTKTGTLOFNTVSKLDTGYSCEARNVGYRRCPCGRMVDLNLISGI 240
QY 241 IAAVVVVVALVISVGLGVCAQRKGYFSKETSFKQSNSSSKATTMSENVQMLTPVIPALW 300
DB 241 IAAVVVVVALVISVGLGVCAQRKGYFSKETSFKQSNSSSKATTMSENVQMLTPVIPALW 300
QY 301 KAAAGSGRGQEF 312
DB 301 KAAAGSGRGQEF 312

RESULT 7
US-09-904-920A-64
Sequence 64, Application US/09904920A
Patent No. 6806352
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,920A
CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15

;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 64
;; LENGTH: 312
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-904-920A-64

Query Match 100.0%; Score 1605; DB 2; Length 312;
Best Local Similarity 100.0%; Pred. No. 1e-148;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARRSHRLLLLLLRYLVVALGYHKAYGFSAPKDDQVVTAVEYQEAAILACKTPKKTYSR 60
DB 1 MARRSHRLLLLLLRYLVVALGYHKAYGFSAPKDDQVVTAVEYQEAAILACKTPKKTYSR 60
QY 61 LEWKLGRSVSFVYQOQTLOGDFKRAEMIDFNIRIKNTRSDAGKYRCEVSAPSEQQN 120
DB 61 LEWKLGRSVSFVYQOQTLOGDFKRAEMIDFNIRIKNTRSDAGKYRCEVSAPSEQQN 120
QY 121 LEEDTTLVLVAPVSPCEVSSALSGTVVLRCDKGNPAPEYTFWFKDGIIRLENPR 180
DB 121 LEEDTTLVLVAPVSPCEVSSALSGTVVLRCDKGNPAPEYTFWFKDGIIRLENPR 180
QY 181 LGSQSTNSSTYNTMTKTGTLQFNVTSKLDTGEYSCEARNVGVYRRCPGRMQVDDNLISGI 240
DB 181 LGSQSTNSSTYNTMTKTGTLQFNVTSKLDTGEYSCEARNVGVYRRCPGRMQVDDNLISGI 240
QY 241 IAAVVVALVISVGLGVCYAKRGYFSKETSFOKSNSSSKATTMSENVQWLTPVIPALW 300
DB 241 IAAVVVALVISVGLGVCYAKRGYFSKETSFOKSNSSSKATTMSENVQWLTPVIPALW 300
QY 301 KAAAGSGRGOEF 312
DB 301 KAAAGSGRGOEF 312

RESULT 8

US-09-909-064-64
; Sequence 64, Application US/09909064
; Patent No. 6818449
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashtenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.

;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth, J.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Mather, Jennie P.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William, I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: 10466-14
;; CURRENT APPLICATION NUMBER: US/09/909,064
;; CURRENT FILING DATE: 2001-07-18
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: 2000-02-22
;; PRIOR APPLICATION NUMBER: US 60/143,048
;; PRIOR FILING DATE: 1999-07-07
;; PRIOR APPLICATION NUMBER: US 60/145,698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: US 60/146,222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 64
;; LENGTH: 312
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-909-064-64

Query Match 100.0%; Score 1605; DB 2; Length 312;
Best Local Similarity 100.0%; Pred. No. 1e-148;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARRSHRLLLLLLRYLVVALGYHKAYGFSAPKDDQVVTAVEYQEAAILACKTPKKTYSR 60
DB 1 MARRSHRLLLLLLRYLVVALGYHKAYGFSAPKDDQVVTAVEYQEAAILACKTPKKTYSR 60
QY 61 LEWKLGRSVSFVYQOQTLOGDFKRAEMIDFNIRIKNTRSDAGKYRCEVSAPSEQQN 120
DB 61 LEWKLGRSVSFVYQOQTLOGDFKRAEMIDFNIRIKNTRSDAGKYRCEVSAPSEQQN 120
QY 121 LEEDTTLVLVAPVSPCEVSSALSGTVVLRCDKGNPAPEYTFWFKDGIIRLENPR 180
DB 121 LEEDTTLVLVAPVSPCEVSSALSGTVVLRCDKGNPAPEYTFWFKDGIIRLENPR 180

QY 181 LGSQSTNSSYTMNTKTGTLOFNTVSKLDTGEYSCEARNVGYRCPGKRMQVDDLNISGI 240
Db 181 LGSQSTNSSYTMNTKTGTLOFNTVSKLDTGEYSCEARNVGYRCPGKRMQVDDLNISGI 240
QY 241 IAAVVVVVALVISVGLGVCYVAQRKGYSKETSFOKNSNSSKATTMSENVQWLTVPVIALW 300
Db 241 IAAVVVVVALVISVGLGVCYVAQRKGYSKETSFOKNSNSSKATTMSENVQWLTVPVIALW 300
QY 301 KAAAGGSRGQEF 312
Db 301 KAAAGGSRGQEF 312

RESULT 9
US-09-905-381A-64
; Sequence 64, Application US/09905381A
; Patent No. 6818746
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,381A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565

; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-905-381A-64

Query Match 100.0%; Score 1605; DB 2; Length 312;
Best Local Similarity 100.0%; Pred. No. 1e-148;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARRSRHRLLLRLVVALGYHKA YGFSAPKDDQVVTA VEYQAILACKTPKKTSSR 60
Db 1 MARRSRHRLLLRLVVALGYHKA YGFSAPKDDQVVTA VEYQAILACKTPKKTSSR 60
QY 61 LEWKLGSRVSFVYYQOTLQDGFKNRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEQGN 120
Db 61 LEWKLGSRVSFVYYQOTLQDGFKNRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEQGN 120
QY 121 LEEDTTLVLVAPVAPSPCEVPSSALSGTVVELRCQKEGNPAPEYTFWKDGIRLLENPR 180
Db 121 LEEDTTLVLVAPVAPSPCEVPSSALSGTVVELRCQKEGNPAPEYTFWKDGIRLLENPR 180
QY 181 LGSQSTNSSYTMNTKTGTLOFNTVSKLDTGEYSCEARNVGYRCPGKRMQVDDLNISGI 240
Db 181 LGSQSTNSSYTMNTKTGTLOFNTVSKLDTGEYSCEARNVGYRCPGKRMQVDDLNISGI 240
QY 241 IAAVVVVVALVISVGLGVCYVAQRKGYSKETSFOKNSNSSKATTMSENVQWLTVPVIALW 300
Db 241 IAAVVVVVALVISVGLGVCYVAQRKGYSKETSFOKNSNSSKATTMSENVQWLTVPVIALW 300
QY 301 KAAAGGSRGQEF 312
Db 301 KAAAGGSRGQEF 312

RESULT 10
US-09-906-618-64
; Sequence 64, Application US/09906618
; Patent No. 6828146
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel

	Matches	312;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps
Qy	1	MARRSRHRLLLLRLLRVLVALGYHKAYGFSAPKQQVVTAVEYQEAILACKTPKKTSSR	60						
Dd	1	MARRSRHRLLLLRLLRVLVALGYHKAYGFSAPKQQVVTAVEYQEAILACKTPKKTSSR	60						
Qy	61	LEWKKLGSRVSFVYYQOTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCVPSAQOQN	120						
Dd	61	LEWKKLGSRVSFVYYQOTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCVPSAQOQN	120						
Qy	121	LEEDTIVTEVLVAVPVPSCVPSALSSTVVVELRCQDKEGNPAPETVTFKDGIRILENPR	180						
Dd	121	LEEDTIVTEVLVAVPVPSCVPSALSSTVVVELRCQDKEGNPAPETVTFKDGIRILENPR	180						
Qy	181	LGSQSTNSSYTMTKTGTLOFTNTVSKLDTGYSCEARNSGVYRRCPGRMQVDDLNISGI	240						
Dd	181	LGSQSTNSSYTMTKTGTLOFTNTVSKLDTGYSCEARNSGVYRRCPGRMQVDDLNISGI	240						
Qy	241	IAAUVVVALVISVCGGLGCVCVAQRKGYSKETSFOKSNSSSKATTMSENVQMLTPVIPALW	300						
Dd	241	IAAUVVVALVISVCGGLGCVCVAQRKGYSKETSFOKSNSSSKATTMSENVQMLTPVIPALW	300						
Qy	301	KAAAGSGRGQEF 312							
Dd	301	KAAAGSGRGQEF 312							

RESULT 13
US-09-904-462-64
; Sequence 64, Application US/09904462
; Patent No. 6878807
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,462
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594

APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,736A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 64
LENGTH: 312
TYPE: PRT
ORGANISM: Homo sapiens
US-09-904-462-64

Query Match 100.0%; Score 1605; DB 2; Length 312;
Best Local Similarity 100.0%; Pred. No. 1e-148;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARRSRHRLLLRLVVALGVHKAQFSAKQDQVTVAVYQEAAILACKTPKKTVSSR 60
Db 1 MARRSRHRLLLRLVVALGVHKAQFSAKQDQVTVAVYQEAAILACKTPKKTVSSR 60
QY 61 LEWKGLGRSVFVYQQTLCQDFKRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEQQN 120
Db 61 LEWKGLGRSVFVYQQTLCQDFKRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEQQN 120
QY 121 LEEDVTTLVLVAPVPSCEVSSALSGTVVBLRCQDKEGNPAPEYTFWFKGIRLLENPR 180
Db 121 LEEDVTTLVLVAPVPSCEVSSALSGTVVBLRCQDKEGNPAPEYTFWFKGIRLLENPR 180
QY 181 LGSQSTNSYTNMTKGTLCQDFKRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEQQN 240
Db 181 LGSQSTNSYTNMTKGTLCQDFKRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEQQN 240
QY 241 TAAVVVVALVSVCGIGVCYAQRKGYFSKETSFKQSNSSSKATTMSENVQWLTTPVIPALW 300
Db 241 TAAVVVVALVSVCGIGVCYAQRKGYFSKETSFKQSNSSSKATTMSENVQWLTTPVIPALW 300
QY 301 KAAAGSGRQGEF 312
Db 301 KAAAGSGRQGEF 312

RESULT 14
US-09-902-736A-64
Sequence 64, Application US/09902736A
Patent No. 6894148
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen

Query Match 100.0%; Score 1605; DB 2; Length 312;
Best Local Similarity 100.0%; Pred. No. 1e-148;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARRSRHRLLLRLVVALGVHKAQFSAKQDQVTVAVYQEAAILACKTPKKTVSSR 60
Db 1 MARRSRHRLLLRLVVALGVHKAQFSAKQDQVTVAVYQEAAILACKTPKKTVSSR 60
QY 61 LEWKGLGRSVFVYQQTLCQDFKRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEQQN 120

Db 61 LEWKLGSRVSFVYQOTLQDGFKNRAEMIDFNIRIKNVTRSDAGKRCVSPSEOGQN 120
Qy 121 LEEDTVTLVLVAPVSPCEVPSSALSGTVVLELRCQDKEGNPAPEYTWFKDGIRLLENPR 180
Db 121 LEEDTVTLVLVAPVSPCEVPSSALSGTVVLELRCQDKEGNPAPEYTWFKDGIRLLENPR 180
Qy 181 LGSOSTNSSYTMNTKTGTLOFNTVSKLDTGEYSCEARNVGYRRCPCGRMVDLNLISGI 240
Db 181 LGSOSTNSSYTMNTKTGTLOFNTVSKLDTGEYSCEARNVGYRRCPCGRMVDLNLISGI 240
Qy 241 IAAVVVVALVISVCGLGVCYAQRKGYSKETSFOKSNSSSKATTMSENVQWLTPVLPALW 300
Db 241 IAAVVVVALVISVCGLGVCYAQRKGYSKETSFOKSNSSSKATTMSENVQWLTPVLPALW 300
Qy 301 KAAAGSGRGOEF 312
Db 301 KAAAGSGRGOEF 312

RESULT 15

US-09-906-722A-64

; Sequence 64, Application US/09906722A
; Patent No. 6946262
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Aeshkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: KJavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: GNE.1618P2C61
; CURRENT APPLICATION NUMBER: US/09/906,722A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-722A-64

Query Match 100.0%; Score 1605; DB 2; Length 312;
Best Local Similarity 100.0%; Pred. No. 1e-148;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARRSRHRLALLRLYLVALGKAYGFSAPKDDQVVTAVEYQEAAILACKTPKKTSSR 60
Db 1 MARRSRHRLALLRLYLVALGKAYGFSAPKDDQVVTAVEYQEAAILACKTPKKTSSR 60
Qy 61 LEWKLGSRVSFVYQOTLQDGFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEOGQN 120
Db 61 LEWKLGSRVSFVYQOTLQDGFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEOGQN 120
Qy 121 LEEDTVTLVLVAPVSPCEVPSSALSGTVVLELRCQDKEGNPAPEYTWFKDGIRLLENPR 180
Db 121 LEEDTVTLVLVAPVSPCEVPSSALSGTVVLELRCQDKEGNPAPEYTWFKDGIRLLENPR 180
Qy 181 LGSOSTNSSYTMNTKTGTLOFNTVSKLDTGEYSCEARNVGYRRCPCGRMVDLNLISGI 240
Db 181 LGSOSTNSSYTMNTKTGTLOFNTVSKLDTGEYSCEARNVGYRRCPCGRMVDLNLISGI 240
Qy 241 IAAVVVVALVISVCGLGVCYAQRKGYSKETSFOKSNSSSKATTMSENVQWLTPVLPALW 300
Db 241 IAAVVVVALVISVCGLGVCYAQRKGYSKETSFOKSNSSSKATTMSENVQWLTPVLPALW 300
Qy 301 KAAAGSGRGOEF 312
Db 301 KAAAGSGRGOEF 312

Search completed: April 10, 2007, 16:33:37
Job time : 67 secs

OM protein - protein search, using sw model
 Run on: April 10, 2007, 16:31:05 ; Search time 52 Seconds
 (without alignments)
 525.184 Million cell updates/sec

Title: US-10-785-221A-9
 Perfect score: 1605
 Sequence: 1 MARRSHRLLLLRLYLVA.....TPVIPALWKAAGSGRQEF 312
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 650591 seqs, 87530628 residues
 Total number of hits satisfying chosen parameters: 650591
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 1500 summaries
 Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1	100.0%;	Score 1605;	DB 2;	Length 312;		
Query Match	100.0%;	Score 1605;	DB 2;	Length 312;		
Best Local Similarity	100.0%;	Pred. No. 1e-148;				
RESULT 2	100.0%;	Score 1605;	DB 2;	Length 312;		
Query Match	100.0%;	Score 1605;	DB 2;	Length 312;		
Best Local Similarity	100.0%;	Pred. No. 1e-148;				
RESULT 3	100.0%;	Score 1605;	DB 2;	Length 312;		
Query Match	100.0%;	Score 1605;	DB 2;	Length 312;		
Best Local Similarity	100.0%;	Pred. No. 1e-148;				
RESULT 4	100.0%;	Score 1605;	DB 2;	Length 312;		
Query Match	100.0%;	Score 1605;	DB 2;	Length 312;		
Best Local Similarity	100.0%;	Pred. No. 1e-148;				
RESULT 5	100.0%;	Score 1605;	DB 2;	Length 312;		
Query Match	100.0%;	Score 1605;	DB 2;	Length 312;		
Best Local Similarity	100.0%;	Pred. No. 1e-148;				
RESULT 6	100.0%;	Score 1605;	DB 2;	Length 312;		
Query Match	100.0%;	Score 1605;	DB 2;	Length 312;		
Best Local Similarity	100.0%;	Pred. No. 1e-148;				
RESULT 7	100.0%;	Score 1605;	DB 2;	Length 312;		
Query Match	100.0%;	Score 1605;	DB 2;	Length 312;		
Best Local Similarity	100.0%;	Pred. No. 1e-148;				
RESULT 8	100.0%;	Score 1605;	DB 2;	Length 312;		
Query Match	100.0%;	Score 1605;	DB 2;	Length 312;		
Best Local Similarity	100.0%;	Pred. No. 1e-148;				
RESULT 9	100.0%;	Score 1605;	DB 2;	Length 312;		
Query Match	100.0%;	Score 1605;	DB 2;	Length 312;		
Best Local Similarity	100.0%;	Pred. No. 1e-148;				
RESULT 10	100.0%;	Score 1605;	DB 2;	Length 312;		
Query Match	100.0%;	Score 1605;	DB 2;	Length 312;		
Best Local Similarity	100.0%;	Pred. No. 1e-148;				
RESULT 11	100.0%;	Score 1605;	DB 2;	Length 312;		
Query Match	100.0%;	Score 1605;	DB 2;	Length 312;		
Best Local Similarity	100.0%;	Pred. No. 1e-148;				
RESULT 12	100.0%;	Score 1605;	DB 2;	Length 312;		
Query Match	100.0%;	Score 1605;	DB 2;	Length 312;		
Best Local Similarity	100.0%;	Pred. No. 1e-148;				
RESULT 13	100.0%;	Score 1605;	DB 2;	Length 312;		
Query Match	100.0%;	Score 1605;	DB 2;	Length 312;		
Best Local Similarity	100.0%;	Pred. No. 1e-148;				
RESULT 14	100.0%;	Score 1605;	DB 2;	Length 312;		
Query Match	100.0%;	Score 1605;	DB 2;	Length 312;		
Best Local Similarity	100.0%;	Pred. No. 1e-148;				
RESULT 15	100.0%;	Score 1605;	DB 2;	Length 312;		
Query Match	100.0%;	Score 1605;	DB 2;	Length 312;		
Best Local Similarity	100.0%;	Pred. No. 1e-148;				

OM protein - protein search, using sw model
Run on: April 10, 2007, 16:41:26 ; Search time 626 Seconds
(without alignments)
761.039 Million cell updates/sec

Title: US-10-785-221A-9
Perfect score: 1605
Sequence: 1 MARRSRHRLLLRLYLVA.....TPVIPALWKAAGSGRQEF 312
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 8366291 seqs, 1526956180 residues
Total number of hits satisfying chosen parameters: 8366291
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match Length	DB	ID	Description
-----	-------	--------------	----	----	-------------

OM protein - protein search, using sw model
Run on: April 10, 2007, 16:46:26 ; Search time 174 Seconds
(without alignments)
759.125 Million cell updates/sec

Title: US-10-785-221A-9
Perfect score: 1605
Sequence: 1 MARRSRHRLLLLLLLRYLVVA.....TPVIPALWKAAGSGRQGEF 312
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1768980 segs, 423358224 residues
Total number of hits satisfying chosen parameters: 1768980
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match Length	DB	ID	Description
-----	-------	--------------	----	----	-------------

GenCore version 6.2
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OM protein - protein search, using sw model

Run on: April 10, 2007, 16:32:55 ; Search time 42 Seconds
(without alignments)
714.753 Million cell updates/sec

Title: US-10-785-221a-9

Perfect score: 1605

Sequence: 1 MARRSRHRLLLRLYLVA.....TPVIPALWKAAGSGRQEF 312

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 1500 summaries

Database :

PIR 80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	404	25.2	299	2 S56749	junctional adhesio
2	206.5	12.9	365	2 JC7780	coxsackie- and ade
3	184	11.5	811	2 A41054	fasciclin II, tran
4	184	11.5	873	2 B41054	fasciclin II, PI-1
5	177	11.0	6642	2 T29757	protein UNC-89 - C
6	169.5	10.6	7962	2 I38346	elastic titin - hu
7	162	10.1	725	2 JE0100	neural cell adhesi
8	162	10.1	1367	2 A41228	protein-tyrosine k
9	161	10.0	344	2 A27681	nonspecific cross-
10	158	9.8	1092	1 JN0635	neural cell adhesi
11	157	9.8	860	2 JC5702	ErbB kinase activa
12	157	9.8	868	2 JC5701	ErbB kinase activa
13	156	9.7	1897	1 TDHULK	leukocyte antigen-
14	155.5	9.7	1328	2 T23007	hypothetical prote
15	155.5	9.7	2783	2 T34416	hypothetical prote
16	155	9.7	521	2 JC1508	biliary glycoprote
17	155	9.7	725	2 JE0099	neural cell adhesi
18	155	9.7	850	2 JC5700	ErbB kinase activa
19	155	9.7	1088	1 IJXJNL	neural cell adhesi
20	154.5	9.6	1323	2 PN0568	connectin 3B - chi
21	154.5	9.6	4391	2 A38096	perlecan precursor
22	153	9.5	4162	2 T42633	connectin/titin -
23	152.5	9.5	1091	1 IJCHNL	neural cell adhesi
24	152	9.5	1033	2 S19247	cell adhesion prot
25	152	9.5	1239	1 A32579	neuroglian - fruit
26	152	9.5	5175	2 T20992	hypothetical prote
27	152	9.5	5198	2 T43290	hemecten precurs
28	151.5	9.4	352	2 T33433	hypothetical prote
29	151.5	9.4	521	2 S34338	biliary glycoprote

30	151.5	9.4	761	1	IJHUNG
31	151.5	9.4	1240	2	T03097
32	151	9.4	773	2	T46283
33	150.5	9.4	519	2	A44783
34	150.5	9.4	1051	2	A39712
35	150.5	9.4	1199	2	T23005
36	150	9.3	1501	2	I58148
37	150	9.3	1863	2	S46217
38	150	9.3	1898	2	S46216
39	149.5	9.3	349	2	A34815
40	149	9.3	1277	2	T30532
41	149	9.3	1499	2	T50212
42	149	9.3	1907	2	S50893
43	148	9.2	858	1	IJRTNC
44	148	9.2	1379	2	JC4954
45	147.5	9.2	333	2	A31923
46	147.5	9.2	1912	2	A56178
47	147	9.2	458	1	MMMSR1
48	146.5	9.1	1612	2	T30805
49	146.5	9.1	1651	2	T14160
50	146	9.1	417	2	JH0394
51	146	9.1	464	2	C30127
52	146	9.1	526	1	A32164
53	145	9.0	764	2	A49448
54	145	9.0	853	1	IJBONC
55	144.5	9.0	423	2	T29549
56	144.5	9.0	1273	2	T42405
57	144.5	9.0	3707	2	S18252
58	144	9.0	725	1	IJMSNG
59	144	9.0	1115	1	IJMSNG
60	143.5	8.9	458	2	JC1509
61	143	8.9	702	2	A36319
62	142.5	8.9	265	2	A55811
63	142.5	8.9	1256	2	T03096
64	142.5	8.9	1894	2	C54689
65	142	8.8	458	2	S68177
66	142	8.8	847	2	JH0371
67	141.5	8.8	344	2	T56551
68	141	8.8	296	2	S01441
69	141	8.8	458	2	S23969
70	141	8.8	647	2	A35648
71	141	8.8	862	2	T49583
72	141	8.8	868	2	A46512
73	141	8.8	2051	2	T30938
74	140.5	8.8	946	1	A47299
75	140	8.7	1262	1	B48758
76	140	8.7	1496	1	A48758
77	139	8.7	477	1	T73631
78	139	8.7	822	1	A56853
79	138.5	8.6	483	2	T17346
80	138.5	8.6	1375	2	T13822
81	138.5	8.6	1526	2	T13823
82	138	8.6	797	2	S38579
83	137	8.5	351	2	JH0396
84	137	8.5	1344	2	T14316
85	136.5	8.5	476	1	A35104
86	136.5	8.5	821	1	S06943
87	136	8.5	526	2	A37821
88	136	8.5	1906	1	S68235
89	135.5	8.4	474	1	C39667
90	135.5	8.4	1091	2	S01998
91	135.5	8.4	1227	2	T23004
92	135	8.4	338	1	JC4776
93	134.5	8.4	476	1	B39667
94	134.5	8.4	814	1	A39752
95	134.5	8.4	821	1	A39667
96	134.5	8.4	1028	2	A53449
97	134.5	8.4	1336	2	T60598
98	133.5	8.3	812	1	A36477
99	133.5	8.3	1070	2	JC4593
100	133.5	8.3	1427	2	T51669
101	133	8.3	919	2	T32541
102	133	8.3	947	1	B44294

neural cell adhesi
CDO protein - huma
hypothetical prote
ecto-ATPase precu
kinase-like protei
hypothetical prote
protein-tyrosine-p
protein-tyrosine-p
leukocyte antigen-
carcinoembryonic a
neural cell adhesi
protein-tyrosine-p
protein-tyrosine-p
neural cell adhesi
vascular endotheli
amalgam protein pr
protein-tyrosine-p
biliary glycoprote
dutt1 protein - mo
transmembrane rece
transmembrane carc
biliary glycoprote
irregular chiasm C
neural cell adhesi
hypothetical prote
sax-3 protein - Ca
heparan sulfate pr
neural cell adhesi
neural cell adhesi
biliary glycoprote
carcinoembryonic a
carcinoembryonic a
CDO protein - rat
protein-tyrosine-p
C-CAM2a protein is
B-cell adhesion pr
neurotrimin - rat
class II histocomp
cell-adhesion mole
B-cell adhesion pr
differentiation an
CD22 homolog/B lym
receptor tyrosine
ror-related recept
protein-tyrosine-p
protein-tyrosine-p
brain-derived neur
brain-derived neur
hypothetical prote
frazzled gene prot
frazzled gene prot
fibroblast growth
biliary glycoprote
rig-1 protein - mo
brain-derived neur
brain-derived neur
myosin-light-chain
myosin-light-chain
brain-derived neur
contactin precurs
hypothetical prote
limbic-system-asso
brain-derived neur
fibroblast growth
brain-derived neur
plasmacytoma-asso
Fit-1 tyrosine kin
fibroblast growth
protein-tyrosine k
tumor suppressor -
unc-5 protein - Ca
unc-5 protein, lon

103	132.5	8.3	321	2	JH0395	biliary glycoprote	176	121.5	7.6	428	2	JS0032	pregnancy-specific
104	132.5	8.3	800	1	TVH02F	fibroblast growth	177	121.5	7.6	435	2	D33258	pregnancy-specific
105	132.5	8.3	800	2	A48991	heparin-binding gr	178	121.5	7.6	816	2	A49151	fibroblast growth
106	132.5	8.3	801	2	J55363	fibroblast growth	179	121.5	7.6	898	2	A40114	fasciclin II precu
107	132.5	8.3	1356	2	JC1402	protein-tyrosine k	180	121	7.5	182	2	A34647	pregnancy-specific
108	132	8.2	1333	2	I79875	receptor tyrosine	181	121	7.5	361	2	FN0020	fibroblast growth
109	132	8.2	1348	2	S51656	vascular endotheli	182	121	7.5	769	2	S16236	fibroblast growth
110	131.5	8.2	309	2	I49522	gene B7-2 protein	183	121	7.5	822	2	A45081	fibroblast growth
111	131.5	8.2	538	2	JC2457	vascular cell adhe	184	121	7.5	822	2	A41794	keratinocyte growt
112	131.5	8.2	976	2	J29583	hypothetical prote	185	121	7.5	832	2	JH0393	fibroblast growth
113	131.5	8.2	1015	2	T32186	hypothetical prote	186	121	7.5	1018	2	JC4211	neural adhesion pr
114	131	8.2	1036	2	S22383	axomin 1 precursor	187	120.5	7.5	799	2	S18209	fibroblast growth
115	129	8.0	769	1	QRRTGS	secretory componen	188	120.5	7.5	821	1	TVH0F2	fibroblast growth
116	129	8.0	871	1	I48696	protein-tyrosine k	189	120.5	7.5	2222	2	T13924	sdk protein - frui
117	129	8.0	881	1	I48697	protein-tyrosine k	190	120	7.5	238	2	T22098	hypothetical prote
118	129	8.0	1535	2	S46224	peroxidasin - frui	191	120	7.5	335	2	C43514	pregnancy-specific
119	129	8.0	6831	2	A88852	protein unc-22 [lim	192	120	7.5	662	2	C40862	heparin-binding gr
120	129	8.0	6839	2	S57242	twitchin [similar]	193	120	7.5	822	1	TVH0FG	fibroblast growth
121	129	8.0	7160	2	T27935	hypothetical prote	194	120	7.5	822	1	TVMSFG	fibroblast growth
122	128.5	8.0	272	2	I48268	biliary glycoprote	195	120	7.5	822	2	I49289	fibroblast growth
123	128.5	8.0	480	2	B56182	fibroblast growth	196	120	7.5	822	2	S29840	fibroblast growth
124	128.5	8.0	757	2	I45956	polymeric immunogl	197	119.5	7.4	286	2	A28333	carcinoembryonic a
125	128.5	8.0	772	2	T13078	KIAA0992 protein -	198	119.5	7.4	309	2	I49503	B-lymphocyte activ
126	128	8.0	1363	2	I58375	protein-tyrosine k	199	119.5	7.4	338	2	JC1238	opioid-binding pro
127	127.5	7.9	1232	2	T43027	neural cell adhesi	200	119.5	7.4	345	2	JC1239	opioid-binding pro
128	126.5	7.9	212	2	C33258	pregnancy-specific	201	119	7.4	310	2	JL0119	Fc gamma (IGG) rec
129	126.5	7.9	419	2	B54312	pregnancy-specific	202	119	7.4	323	2	S06946	Fc gamma (IGG) rec
130	126.5	7.9	419	2	JC4123	pregnancy-specific	203	119	7.4	707	2	A54846	fibroblast growth
131	126.5	7.9	875	2	T33434	hypothetical prote	204	119	7.4	765	2	C42632	cell adhesion mole
132	126.5	7.9	1447	2	A54100	tumor suppressor p	205	119	7.4	812	2	B42632	cell adhesion mole
133	126	7.9	228	2	S29575	Ig light chain - r	206	119	7.4	932	2	A42632	cell adhesion mole
134	126	7.9	338	2	JC5519	50K glycoprotein p	207	119	7.4	1018	2	A54744	contactin 1 precu
135	126	7.9	1338	2	S09982	protein-tyrosine k	208	119	7.4	3488	2	T34418	hypothetical prote
136	125.5	7.8	326	2	JC4124	pregnancy-specific	209	118.5	7.4	254	2	C42691	fibroblast growth
137	125.5	7.8	341	2	JC1512	biliary glycoprote	210	118.5	7.4	282	2	T17219	hypothetical prote
138	125.5	7.8	352	2	I77374	pregnancy-specific	211	118.5	7.4	317	2	JL0118	Fc gamma (IGG) rec
139	125.5	7.8	480	2	A56182	fibroblast growth	212	118.5	7.4	646	2	I38049	cell surface glyco
140	125.5	7.8	806	1	TVH0F3	fibroblast growth	213	118.5	7.4	739	2	A41288	vascular cell adhe
141	125	7.8	1197	2	T30581	neural cell adhesi	214	118.5	7.4	1443	2	I50600	neogenin - chicken
142	124.5	7.8	1240	2	JC4122	pregnancy-specific	215	118.5	7.4	1894	2	S50065	sialoadhesin - mou
143	124.5	7.8	235	2	S20000	Ig light chain pre	216	118.5	7.4	658	2	T13931	projectin - fruit
144	124.5	7.8	395	2	D43354	pregnancy-specific	217	118	7.4	326	2	F43354	pregnancy-specific
145	124.5	7.8	397	2	C43354	pregnancy-specific	218	118	7.4	567	2	S29498	lymphocyte antigen
146	124.5	7.8	406	2	E43354	pregnancy-specific	219	118	7.4	584	2	T08678	hypothetical prote
147	124.5	7.8	417	2	A28277	pregnancy-specific	220	118	7.4	6805	2	S20501	titin - rabbit (fr
148	124.5	7.8	426	2	A35964	pregnancy-specific	221	117.5	7.3	278	2	JC1506	biliary glycoprote
149	124.5	7.8	822	2	B54846	pregnancy-specific	222	117.5	7.3	278	2	A39037	carcinoembryonic a
150	124.5	7.8	1241	2	T37190	nephlin - human	223	117	7.3	509	2	JC5288	SHP substrate-1 pr
151	124	7.7	1028	2	I58164	BIG-1 protein - ra	224	117	7.3	513	2	JC5289	SHP substrate-1 pr
152	124	7.7	1259	2	A43425	Bravo/Nr-CAM cell	225	117	7.3	1040	2	A34695	axonal glycoprotei
153	124	7.7	1268	1	A39640	neural cell adhesi	226	116.5	7.3	333	2	A43354	pregnancy-specific
154	123.5	7.7	273	2	B28928	pregnancy-specific	227	116.5	7.3	345	2	JC4025	opioid-binding cel
155	123.5	7.7	275	2	A28928	pregnancy-specific	228	116.5	7.3	345	2	S03199	opioid-binding pro
156	123.5	7.7	282	2	C28928	pregnancy-specific	229	116.5	7.3	402	2	A54312	pregnancy-specific
157	123.5	7.7	299	2	I46690	CD80 precursor - r	230	116.5	7.3	424	2	B36109	pregnancy-specific
158	123.5	7.7	419	2	A33258	pregnancy-specific	231	116.5	7.3	426	2	C55181	pregnancy-specific
159	123.5	7.7	419	2	A31135	pregnancy-specific	232	116.5	7.3	426	2	B35334	pregnancy-specific
160	123.5	7.7	426	2	B33258	pregnancy-specific	233	116.5	7.3	436	2	B55181	pregnancy-specific
161	123.5	7.7	426	2	A35341	pregnancy-specific	234	116.5	7.3	495	2	A55181	pregnancy-specific
162	123.5	7.7	428	2	A27658	pregnancy-specific	235	116.5	7.3	739	2	J50675	vascular cell adhe
163	123.5	7.7	757	1	S48841	secretory componen	236	116.5	7.3	764	1	QRHUGS	secretory componen
164	123.5	7.7	2626	1	I38344	titin, cardiac mus	237	116.5	7.3	1223	2	S36846	myosin-binding pro
165	123	7.7	1040	2	A49356	transient axonal g	238	116.5	7.3	1265	1	A37967	neural cell adhesi
166	123	7.7	1091	2	A58532	glial cell membran	239	116	7.2	335	2	C54312	pregnancy-specific
167	123	7.7	1330	2	S49010	embryonic receptor	240	116	7.2	335	2	B33251	nonspecific cross-
168	122.5	7.6	419	2	A36109	pregnancy-specific	241	116	7.2	662	2	T16525	hypothetical prote
169	122.5	7.6	1896	2	T08851	Down syndrome cell	242	116	7.2	707	2	A38429	keratinocyte growt
170	122	7.6	682	2	A35969	heparin-binding gr	243	116	7.2	940	2	A40985	projectin - fruit
171	122	7.6	813	1	A49123	fibroblast growth	244	115.5	7.2	324	2	G43354	pregnancy-specific
172	121.5	7.6	233	2	S29577	Ig light chain - r	245	115.5	7.2	335	2	H43354	pregnancy-specific
173	121.5	7.6	332	2	UN0067	pregnancy-specific	246	115.5	7.2	636	2	I61718	neu differentiation
174	121.5	7.6	424	2	A34595	pregnancy-specific	247	115.5	7.2	824	2	S36439	fibroblast growth
175	121.5	7.6	428	2	I57486	pregnancy-specific	248	115.5	7.2	888	2	S23065	ufo protein - mous

249	115.5	7.2	942	2	S23251	protein-tyrosine k	322	106.5	6.6	473	2	D88976	protein F54B2.4 [i
250	115	7.2	351	2	B34595	pregnancy-specific	323	106.5	6.6	538	2	I68093	PRR2 delta - human
251	115	7.2	602	2	A45769	acetylcholine rece	324	106.5	6.6	1011	2	T13669	neuromusculin - fr
252	115	7.2	823	2	B35963	protein-tyrosine k	325	106	6.6	531	2	S20900	titin - mouse (fra
253	115	7.2	824	2	S24108	protein-tyrosine k	326	105.5	6.6	166	2	A33402	pregnancy-specific
254	115	7.2	917	2	I48950	telencephalin prec	327	105.5	6.6	773	1	ORRBG	secretory componen
255	115	7.2	1257	1	A41060	neural cell adhesi	328	105	6.5	240	2	S01299	OX-45 membrane gly
256	115	7.2	1298	2	A48999	protein-tyrosine k	329	104.5	6.5	518	2	JC4024	poliovirus recepto
257	114.5	7.1	413	2	S65949	hemolin - cecropia	330	104.5	6.5	745	2	B43273	heregulin, splice
258	114.5	7.1	426	2	S03016	pregnancy-specific	331	104.5	6.5	789	2	T28714	hypothetical prote
259	114.5	7.1	819	1	TVCHFG	fibroblast growth	332	104.5	6.5	1355	2	T28715	hypothetical prote
260	114.5	7.1	821	1	TVWSBK	fibroblast growth	333	104.5	6.5	1450	2	A44027	165K myofibrillar
261	114	7.1	182	2	I83053	pregnancy-specific	334	104.5	6.5	2029	1	TDFELK	protein-tyrosine-p
262	114	7.1	206	2	A40305	biliary glycoprote	335	104	6.5	336	2	S42632	Fit-1s protein pre
263	114	7.1	1260	1	S05479	neural cell adhesi	336	104	6.5	344	2	A41357	FC gamma (IG) rec
264	114	7.1	1274	1	S55050	cardiac myosin-bin	337	104	6.5	353	2	S51242	heparin-binding fi
265	113.5	7.1	392	1	RWHUPD	poliovirus recepto	338	104	6.5	355	2	I51157	major histocompati
266	113.5	7.1	417	1	RWHUPD	poliovirus recepto	339	104	6.5	374	1	A39878	FC gamma (IG) rec
267	113.5	7.1	524	2	S35341	ketin - fruit fly	340	104	6.5	392	2	B44194	poliovirus recepto
268	113.5	7.1	620	2	JH0593	Schwann cell myeli	341	104	6.5	417	2	A44194	poliovirus recepto
269	113.5	7.1	628	2	I38000	Lutheran blood gro	342	104	6.5	739	2	JN0581	vascular cell adhe
270	113.5	7.1	629	2	A46500	Ly-9.2 antigen - m	343	104	6.5	802	1	TVHUP4	fibroblast growth
271	113.5	7.1	647	2	B41288	vascular cell adhe	344	103.5	6.4	588	2	JH0506	adhesion molecule
272	113.5	7.1	748	2	S41050	fibroblast growth	345	103.5	6.4	588	2	A45254	surface glycoprote
273	113.5	7.1	806	2	A35963	protein-tyrosine k	346	103.5	6.4	818	2	JC4058	fibroblast growth
274	113.5	7.1	976	1	TVMSMD	macrophage colony-	347	103	6.4	309	2	S15674	cell surface glyco
275	113.5	7.1	1021	2	A57112	contactin precursor	348	103	6.4	650	1	JC1450	fibroblast growth
276	113	7.0	626	1	A61084	myelin-associated	349	103	6.4	1666	2	A48594	skelemin - mouse
277	113	7.0	705	2	S51635	fibroblast growth	350	103	6.4	2295	2	C88369	protein unc-52 [im
278	113	7.0	1173	2	T25893	hypothetical prote	351	103	6.4	3375	2	T19821	hypothetical prote
279	113	7.0	1259	2	S36126	neural cell adhesi	352	102.5	6.4	255	2	JC7593	SH2 domain-contain
280	112.5	7.0	288	2	A45803	B-cell-restricted	353	102.5	6.4	278	2	JC1507	biliary glycoprote
281	112.5	7.0	733	2	I49293	fibroblast growth	354	102.5	6.4	508	2	A33378	fasciclin III prec
282	112.5	7.0	1020	2	S05944	neutonal cell surf	355	102.5	6.4	1176	2	JN0583	myosin-light-chain
283	112.5	7.0	1138	2	S24614	myosin-binding pro	356	102	6.4	336	2	C27658	pregnancy-specific
284	112	7.0	503	2	JC5287	SHP substrate-1 pr	357	102	6.4	362	2	A45897	MHC class I histoc
285	112	7.0	1209	2	T42718	probable neural ce	358	102	6.4	398	2	A39371	Ig V-region-like B
286	111.5	6.9	413	2	A37778	hemolin precursor	359	102	6.4	416	1	A42879	advanced glycosyla
287	111.5	6.9	584	2	I50419	s-gicerin precursor	360	102	6.4	530	2	A53437	poliovirus recepto
288	111.5	6.9	978	2	S16385	macrophage colony-	361	102	6.4	640	2	A43273	heregulin precursor
289	111	6.9	613	4	A40201	artifact-warning s	362	101.5	6.3	270	2	S65739	basigin precursor
290	110.5	6.9	341	2	JC1511	biliary glycoprote	363	101.5	6.3	523	2	I50478	neuroilin - goldfis
291	110.5	6.9	344	1	RWRTC2	T-cell surface gly	364	101.5	6.3	1000	1	I46521	titin - rabbit (fr
292	110.5	6.9	588	2	I37202	B-CAM protein - hu	365	101.5	6.3	1089	1	S33727	platelet-derived g
293	110.5	6.9	729	2	A56795	fibroblast growth	366	101	6.3	462	2	I38404	neu differentiation
294	110	6.9	238	2	S31779	trypsin (EC 3.4.21	367	101	6.3	627	4	A40201	artifact-warning s
295	110	6.9	639	2	I61719	neu differentiation	368	100.5	6.3	372	2	C39371	Ig V-region-like B
296	110	6.9	822	2	B49151	fibroblast growth	369	100.5	6.3	817	2	A48721	titin, muscle - ch
297	109.5	6.8	495	2	T25750	hypothetical prote	370	100	6.2	264	2	T26976	hypothetical prote
298	109.5	6.8	822	2	S19947	fibroblast growth	371	100	6.2	277	2	I52825	gene MAC25 protein
299	109.5	6.8	1021	2	T42634	connectin/titin -	372	100	6.2	282	2	S50031	prostacyclin-stimu
300	109.5	6.8	1040	2	A57638	receptor tyrosine	373	100	6.2	362	2	JH0291	class I histocoma
301	109.5	6.8	1103	2	T22889	hypothetical prote	374	100	6.2	526	2	S70587	butyrophilin precu
302	109	6.8	520	1	S44099	brain-derived neur	375	100	6.2	974	1	A49714	protein-tyrosine k
303	109	6.8	582	1	BNRT3S	myelin-associated	376	99.5	6.2	304	2	B88746	protein C18p3.3 [i
304	109	6.8	626	1	BNRT3	myelin-associated	377	99.5	6.2	209	2	T15747	hypothetical prote
305	109	6.8	637	1	B33785	myelin-associated	378	99.5	6.2	612	2	I73633	gene trkC protein
306	109	6.8	818	1	S44098	brain-derived neur	379	99.5	6.2	825	2	A55178	neurotrophin recep
307	109	6.8	1272	2	S26180	neurofascin - chic	380	99.5	6.2	839	1	I73632	neurotrophin-3 rec
308	109	6.8	1880	2	T18531	tractin - mediana	381	99.5	6.2	1287	2	I30988	hypothetical prote
309	108.5	6.8	339	2	T28138	Ig V-region-like B	382	99	6.2	475	2	T76668	pregnancy-specific
310	108.5	6.8	404	1	I61596	advanced glycosyla	383	99	6.2	874	2	T29548	hypothetical prote
311	108.5	6.8	487	2	S65133	butyrophilin - mou	384	98.5	6.1	268	2	T23555	hypothetical prote
312	108	6.7	340	2	T28137	Ig V-region-like B	385	98.5	6.1	422	2	S32357	glial growth facto
313	108	6.7	799	1	TVRTTB	nerve growth facto	386	98.5	6.1	738	2	A40096	platelet-endotheli
314	107.5	6.7	637	2	C43273	heregulin precursor	387	98.5	6.1	1327	2	T09402	immunoglobulin-lik
315	107.5	6.7	662	2	I61722	neu differentiation	388	98.5	6.1	1462	1	B36182	protein-tyrosine-p
316	107.5	6.7	750	2	S41051	fibroblast growth	389	98	6.1	240	2	JL0143	antigen BCM1 precu
317	107	6.7	267	2	A38442	probable tumor sup	390	98	6.1	356	2	JH0289	class I histocoma
318	107	6.7	599	2	T16774	hypothetical prote	391	98	6.1	583	2	I39428	alcam - human
319	107	6.7	820	2	S17295	fibroblast growth	392	98	6.1	1052	2	B49120	protein-tyrosine k
320	106.5	6.6	289	2	G00031	B7 protein - red-c	393	98	6.1	1088	1	PFRTGA	platelet-derived g
321	106.5	6.6	391	2	T09058	butyrophilin homol	394	98	6.1	1142	2	S36845	myosin-binding pro

395	98	6.1	1191	2	S35305	zinc finger protei	468	89.5	5.6	354	1	LKHU	proteoglycan link
396	97.5	6.1	421	2	T46266	hypothetical prote	469	89.5	5.6	618	2	T08685	hypothetical prote
397	97.5	6.1	960	1	JN0677	protein-tyrosine k	470	89	5.5	219	2	PC4203	Ig kappa chain (mo
398	97.5	6.1	1451	2	S42167	190K protein - hum	471	89	5.5	230	2	A56210	neu differentiation
399	97	6.0	362	2	JH0292	class I histocompa	472	89	5.5	264	2	I46020	FC gamma 2 recepto
400	97	6.0	978	1	A49814	protein-tyrosine k	473	89	5.5	339	2	JC7509	glycoprotein Vi-1
401	97	6.0	1147	2	A59307	protein-tyrosine k	474	89	5.5	347	2	S41638	T-cell surface gly
402	96.5	6.0	370	2	S29139	aggreccan - pig (fr	475	89	5.5	362	2	JH0288	class I histocompa
403	96.5	6.0	1244	2	T49632	hypothetical prote	476	89	5.5	510	2	PC4054	cardiac C-protein
404	96	6.0	304	1	RWCHH7	cell surface glyco	477	89	5.5	980	1	TVCTMD	macrophage colony-
405	96	6.0	687	2	A49636	soluble vascular e	478	88.5	5.5	348	2	I68745	MHC class I lympho
406	96	6.0	713	2	I50128	fibroblast growth	479	88.5	5.5	1021	2	I39207	leukocyte surface
407	96	6.0	829	2	JC4583	fibroblast growth	480	88.5	5.5	1592	2	T16055	hypothetical prote
408	96	6.0	894	1	A41527	protein-tyrosine k	481	88.5	5.5	1723	2	H86557	polymorphic membra
409	96	6.0	999	2	I38547	novel cellular pro	482	88.5	5.5	1723	2	E72067	polymorphic membra
410	95.5	6.0	240	2	JC4121	pregnancy-specific	483	88.5	5.5	1732	2	C81601	polymorphic membra
411	95.5	6.0	269	2	A46506	leukocyte activati	484	88	5.5	255	1	S48146	mucin 1 precursor,
412	95.5	6.0	1132	2	A35089	myosin-binding pro	485	88	5.5	362	2	JH0290	class I histocompa
413	95	5.9	167	2	S29579	Ig light chain - r	486	88	5.5	790	2	A39627	protein-tyrosine k
414	95	5.9	219	2	S52028	Ig kappa chain - r	487	87.5	5.5	666	2	I58169	semaphorin iii - m
415	95	5.9	241	2	D43273	heregulin precurs	488	87	5.4	238	2	A49633	Ig lambda-like cha
416	95	5.9	749	2	G01856	semaphorin V - hum	489	87	5.4	313	2	H36854	hemagglutinin - va
417	94.5	5.9	273	2	JX0107	basigin precursor	490	87	5.4	330	2	I46691	CD86 precursor - r
418	94.5	5.9	321	2	I54766	B-lymphocyte activ	491	87	5.4	342	2	S33355	class I histocompa
419	94.5	5.9	825	1	A40026	neurotrophin-3 rec	492	87	5.4	408	1	LKRT2	proteoglycan link
420	94.5	5.9	890	1	A33743	protein-tyrosine k	493	86.5	5.4	116	2	S20708	Ig kappa chain v r
421	94	5.9	241	2	S32359	glial growth facto	494	86.5	5.4	172	2	B26414	95K nonspecific cr
422	94	5.9	288	2	B45897	MHC class I histoc	495	86.5	5.4	210	2	F82238	phosphoribosyl-AMP
423	94	5.9	697	2	T34006	hypothetical prote	496	86.5	5.4	270	2	A34636	FC-gamma receptor
424	94	5.9	702	2	T21148	hypothetical prote	497	86.5	5.4	274	2	T32736	hypothetical prote
425	94	5.9	1679	2	T30271	surface protein -	498	86.5	5.4	285	2	S36903	FC gamma (IgG) rec
426	93.5	5.8	257	2	PS0401	basigin type II -	499	86.5	5.4	375	2	I60125	PDGF receptor beta
427	93.5	5.8	271	2	S43512	GP42/Basigin prote	500	86.5	5.4	707	2	JC7763	neural leucine-r
428	93.5	5.8	275	2	PS0402	basigin type III -	501	86	5.4	220	2	A49444	Ig gamma-1 heavy c
429	93.5	5.8	345	2	A46052	vascular cell adhe	502	86	5.4	243	2	A37982	calcium vector pro
430	93.5	5.8	592	2	S25705	Ig mu chain - shee	503	86	5.4	395	2	T31822	hypothetical prote
431	93.5	5.8	729	2	A49120	fibroblast growth	504	86	5.4	478	2	I53960	PRR2 alpha - human
432	93.5	5.8	876	2	I49152	protein-tyrosine k	505	86	5.4	562	2	G02426	interleukin-1 rece
433	93.5	5.8	880	2	B53743	protein-tyrosine k	506	86	5.4	880	1	JC4166	protein-tyrosine k
434	93.5	5.8	1437	2	T31093	probable protein-t	507	86	5.4	954	2	H97100	DNA gyrase A chain
435	93	5.8	524	2	D82944	hypothetical membr	508	86	5.4	964	2	T15746	hypothetical prote
436	93	5.8	1089	1	PFHUGA	platelet-derived g	509	85.5	5.3	283	1	FCMSG1	FC gamma (IgG) rec
437	92.5	5.8	214	2	S68212	Ig kappa chain (Ma	510	85.5	5.3	302	2	C36484	fibroblast growth
438	92.5	5.8	354	1	S04243	proteoglycan link	511	85.5	5.3	341	2	I51158	major histocompati
439	92.5	5.8	525	1	A58674	neurotrophin-3 rec	512	85.5	5.3	369	2	AB2550	hypothetical prote
440	92.5	5.8	803	1	S35695	neurotrophin-3 rec	513	85.5	5.3	558	2	JC5204	60K cysteine-rich
441	92.5	5.8	818	2	T19120	hypothetical prote	514	85.5	5.3	619	2	S45932	tyrosine transport
442	92.5	5.8	852	2	I51259	receptor tyrosine	515	85.5	5.3	625	2	T16777	hypothetical prote
443	92.5	5.8	882	2	I38912	protein H05009.1 [516	85.5	5.3	1398	2	T25568	hypothetical prote
444	92.5	5.8	2109	2	E89066	genome polyprotein	517	85.5	5.3	1748	1	JN0786	integrin beta-4 ch
445	92.5	5.8	2179	1	GNNYH4	hypothetical prote	518	85.5	5.3	2415	1	A39086	aggreccan precursor
446	92.5	5.8	2541	2	T29340	cag island protein	519	85	5.3	207	2	A56190	titin - rat (fragm
447	92.5	5.8	370	2	C71926	class I histocompa	520	85	5.3	330	2	A40071	Ig kappa chain - m
448	92	5.7	329	2	A40730	probable advanced	521	85	5.3	330	2	A40071	FC gamma (IgG) rec
449	91.5	5.7	402	2	T09062	165K protein, skel	522	85	5.3	330	2	I49660	FC-gamma-1/gamma-2
450	91.5	5.7	402	2	S43529	MHC class II histo	523	85	5.3	362	2	A45849	MHC class I histoc
451	91.5	5.7	1465	2	S43529	DM-GRASP precursor	524	85	5.3	416	2	S33473	interleukin-1 rece
452	91	5.7	265	2	C39797	protein-tyrosine k	525	85	5.3	528	2	T50012	hypothetical prote
453	91	5.7	587	2	JH0464	protein-tyrosine k	526	85	5.3	2013	2	AD1129	probable peptidogl
454	91	5.7	975	1	TVMSTK	C-mer tyrosine kin	527	84.5	5.3	257	2	S00682	IgE Fc receptor al
455	91	5.7	994	2	I49276	proteoglycan link	528	84.5	5.3	532	1	A29849	intercellular adhe
456	90.5	5.6	354	1	S42938	internalin protein	529	84.5	5.3	547	1	S28904	intercellular adhe
457	90.5	5.6	832	2	AD1096	neurotrophic recep	530	84.5	5.3	709	2	A35364	carcinoembryonic a
458	90.5	5.6	937	2	A45082	hypothetical prote	531	84.5	5.3	841	2	JCS894	killer cell inhibi
459	90.5	5.6	1060	2	S63252	proteoglycan core	532	84.5	5.3	876	2	G90592	hypothetical prote
460	90.5	5.6	2124	2	A28452	aggreccan precursor	533	84.5	5.3	896	2	I45858	desmocollin - bovi
461	90.5	5.6	2132	1	A55182	brain link protein	534	84.5	5.3	1005	2	T18537	Ig heavy chain - c
462	90	5.6	340	2	JC7505	methyl-accepting c	535	84.5	5.3	1452	1	S17669	protein-tyrosine-p
463	90	5.6	401	2	E83720	protein dim-1 [imp	536	84.5	5.3	1452	1	S17670	protein-tyrosine-p
464	90	5.6	666	2	H89581	versican precursor	537	84.5	5.3	1778	2	AF1116	aggreccan precursor
465	90	5.6	1643	2	T14274	versican precursor	538	84.5	5.3	2109	1	I50421	phage repressor pr
466	90	5.6	3381	2	T42389	probable lipoprote	539	84	5.2	210	2	AH1039	Ig kappa chain pre
467	89.5	5.6	188	2	E87048		540	84	5.2	225	2	JL0029	

541	84	5.2	275	1	HLHU10	MHC class I histoc	614	80.5	5.0	366	2	I72113	MHC histocompatibi
542	84	5.2	312	2	QJ1862	3IR protein - vari	615	80.5	5.0	366	2	I38507	MHC class I histoc
543	84	5.2	363	2	A45845	MHC class I histoc	616	80.5	5.0	613	2	T27528	hypothetical prote
544	84	5.2	380	2	S12839	Ig heavy chain pre	617	80.5	5.0	905	2	T38944	probable coatomer
545	84	5.2	458	1	RWHUT4	T-cell surface gly	618	80.5	5.0	5147	1	IJFFTM	cadherin-related t
546	84	5.2	1185	2	T46428	hypothetical prote	619	80.5	5.0	13055	2	T16580	hypothetical prote
547	84	5.2	1537	2	S53465	hypothetical prote	620	80	5.0	125	2	S62876	hypothetical prote
548	83.5	5.2	221	2	A82190	floculation prote	621	80	5.0	215	2	JE0243	Ig kappa chain NIG
549	83.5	5.2	229	2	A20969	hypothetical prote	622	80	5.0	247	1	A54662	myelin P0 protein
550	83.5	5.2	238	2	I68699	Ig kappa chain pre	623	80	5.0	283	1	LNFLHS	lectin precursor -
551	83.5	5.2	355	2	B40730	MHC class I histoc	624	80	5.0	292	1	KFRB3	tissue factor prec
552	83.5	5.2	358	2	A28834	internalin protein	625	80	5.0	325	2	I54449	MHC class I HLA-Cx
553	83.5	5.2	388	2	AF1383	interleukin-1 rece	626	80	5.0	355	2	B26883	neural cell adhesi
554	83.5	5.2	398	2	S17428	probable N-carbamyl	627	80	5.0	363	1	S42102	MHC class I histoc
555	83.5	5.2	411	1	D64079	novel antigen rece	628	80	5.0	365	1	HLHUA2	MHC class I histoc
556	83.5	5.2	684	2	S60266	G-quartet DNA bind	629	80	5.0	365	2	I37470	HLA-A*0210 - human
557	83.5	5.2	725	2	T03219	protein-tyrosine k	630	80	5.0	365	2	I84448	MHC class I histoc
558	83.5	5.2	941	1	TVNVM	hypothetical prote	631	80	5.0	365	2	I61857	MHC HLA-A2.4a chai
559	83.5	5.2	436	2	E71086	hypothetical prote	632	80	5.0	399	1	G2MSAM	Ig gamma-2a chain
560	83	5.2	175	2	A39171	T-cell surface gly	633	80	5.0	454	2	F90602	aminopeptidase (le
561	83	5.2	197	2	P00327	heparin-binding fi	634	80	5.0	457	2	A27449	T-cell surface gly
562	83	5.2	240	2	A39016	T-cell surface gly	635	80	5.0	473	2	G96963	pyruvate kinase (p
563	83	5.2	265	2	I38443	gene HLA-A-0203 pr	636	80	5.0	487	2	T28804	hypothetical prote
564	83	5.2	3507	2	T34513	hypothetical prote	637	80	5.0	575	2	C86398	protein TNF9.26 li
565	82.5	5.1	230	2	S33161	Ig kappa chain - s	638	80	5.0	643	2	F84117	hypothetical prote
566	82.5	5.1	351	1	RWHUC2	T-cell surface gly	639	80	5.0	701	2	T19605	hypothetical prote
567	82.5	5.1	439	2	AE1251	probable peptidogl	640	80	5.0	718	2	AB1258	hypothetical prote
568	82.5	5.1	513	2	A71004	hypothetical prote	641	80	5.0	1123	2	T47687	adaptor protein/ a
569	82.5	5.1	987	2	A88746	protein C18f3.2 [1	642	80	5.0	1160	2	F88369	protein unc-52 [im
570	82.5	5.1	1330	2	A36373	hypothetical prote	643	80	5.0	1578	2	AD1512	peptidoglycan bou
571	82.5	5.1	2327	2	T24630	hypothetical prote	644	80	5.0	1871	2	D96698	probable DNA polym
572	82	5.1	194	2	T29925	aggreccan - bovine	645	80	5.0	1894	2	T02155	DNA-directed DNA p
573	82	5.1	205	2	A48929	activated B-cell p	646	80	5.0	1983	2	G86643	hypothetical prote
574	82	5.1	253	2	T15475	hypothetical prote	647	79.5	5.0	234	2	S01320	Ig kappa chain pre
575	82	5.1	267	2	B71062	hypothetical prote	648	79.5	5.0	295	1	KFH03	ctlease factor prec
576	82	5.1	313	2	T28598	hypothetical prote	649	79.5	5.0	323	2	A48997	tumor surface anti
577	82	5.1	352	2	I51541	MHC class I antige	650	79.5	5.0	365	2	A47636	MHC class I histoc
578	82	5.1	356	2	A27797	class I histocompa	651	79.5	5.0	366	2	S42823	MHC class I histoc
579	82	5.1	365	2	I61902	MHC class I histoc	652	79.5	5.0	381	2	I51174	Ig heavy chain - R
580	82	5.1	365	2	I38441	gene HLA-A-6802 pr	653	79.5	5.0	416	2	A54017	colon carcinoma-as
581	82	5.1	365	2	I38442	gene HLA-A-0205 pr	654	79.5	5.0	475	2	A54879	pregnancy-specific
582	82	5.1	370	2	E64587	cag pathogenicity	655	79.5	5.0	568	2	A45804	Ig mu chain C regi
583	82	5.1	411	2	AE1336	probable fibronect	656	79.5	5.0	605	2	S67815	protein-tyrosine k
584	82	5.1	680	2	JCS895	killer cell inhibi	657	79.5	5.0	772	2	I48747	semaphorin D - mou
585	82	5.1	938	2	T01809	hypothetical prote	658	79.5	5.0	811	2	PN0689	connectin 1 - chic
586	82	5.1	1213	2	T19835	hypothetical prote	659	79.5	5.0	830	2	T43999	glycoprotein B [im
587	82	5.1	1256	2	G97902	alpha-amylase (EC	660	79.5	5.0	971	2	C75503	hypothetical prote
588	81.5	5.1	224	2	A56169	Ig kappa chain V r	661	79.5	5.0	972	1	TVHUMD	macrophage colony-
589	81.5	5.1	224	2	I37243	CMRF-35 antigen -	662	79.5	5.0	977	2	I45877	protein-tyrosine k
590	81.5	5.1	236	2	JH0372	42K surface glycop	663	79.5	5.0	1104	2	C72409	reverse gyrase - T
591	81.5	5.1	316	2	D71535	probable NADH (ubi	664	79.5	5.0	1385	2	D89824	hypothetical prote
592	81.5	5.1	355	2	I80169	class I histocompa	665	79.5	5.0	2314	1	A46151	hypothetical prote
593	81.5	5.1	537	2	A35400	surface protein T6	666	79	4.9	135	2	S40342	protein-tyrosine-p
594	81.5	5.1	635	2	JCS896	killer cell inhibi	667	79	4.9	182	2	A25468	Ig kappa chain - h
595	81.5	5.1	1335	2	T17508	glycoprotein Vp260	668	79	4.9	185	2	B70755	T-cell surface gly
596	81	5.0	164	2	T17508	hypothetical prote	669	79	4.9	313	2	I36958	probable lprB prot
597	81	5.0	196	2	T19794	hypothetical prote	670	79	4.9	337	2	I67482	MHC class I heavy
598	81	5.0	276	2	S20690	31.6K hypothetical	671	79	4.9	405	1	G2MSBM	Ig gamma-2b chain
599	81	5.0	290	2	AG2216	hypothetical prote	672	79	4.9	407	2	T08732	hypothetical prote
600	81	5.0	362	2	JH0541	class I histocompa	673	79	4.9	468	2	T40223	HMG-box containing
601	81	5.0	362	2	JH0539	class I histocompa	674	79	4.9	481	2	S26698	alkaline proteinas
602	81	5.0	362	2	JH0540	class I histocompa	675	79	4.9	556	1	S12802	60K cysteine-rich
603	81	5.0	1087	2	I51552	platelet-derived g	676	79	4.9	556	2	A86560	60 kDa Cysteine-ri
604	81	5.0	1286	2	T16507	hypothetical prote	677	79	4.9	582	2	B86366	phosphoglucosidase
605	80.5	5.0	119	2	B27588	Ig kappa chain pre	678	79	4.9	657	2	AD1525	probable cell surf
606	80.5	5.0	178	2	PT0219	Ig kappa chain V-C	679	79	4.9	771	2	D49423	semaphorin III pre
607	80.5	5.0	266	2	A28031	MHC class II histo	680	79	4.9	774	1	QRECEA	iron(III) dicitrat
608	80.5	5.0	329	1	A48754	B7-2 antigen - hum	681	79	4.9	785	2	A29953	alpha-1 proteinase
609	80.5	5.0	335	2	S58892	signaling lymphocy	682	79	4.9	815	2	JG0197	myosin-light-chain
610	80.5	5.0	345	2	I68749	MHC class I lympho	683	79	4.9	871	2	T45692	receptor-like prot
611	80.5	5.0	357	2	I36965	MHC class I protei	684	79	4.9	1014	2	T13476	hypothetical prote
612	80.5	5.0	365	2	S01171	class I histocompa	685	79	4.9	1073	2	T33764	hypothetical prote
613	80.5	5.0	366	2	I37526	MHC class I histoc	686	79	4.9	1684	2	S10789	amylase A-180 - al

687	79	4.9	1922	2	T00637	hypothetical prote	760	77.5	4.8	5291	2	F90696	hypothetical prote
688	78.5	4.9	237	2	G28043	MHC class II histoc	761	77	4.8	219	2	S16112	Ig kappa chain V r
689	78.5	4.9	254	1	JL0107	Fc gamma (IgG) rec	762	77	4.8	265	2	B90242	conserved hypothet
690	78.5	4.9	261	2	S39797	MHC class II DR-be	763	77	4.8	289	2	B86794	hypothetical prote
691	78.5	4.9	318	2	F72171	K9R protein - vari	764	77	4.8	328	2	I47160	Ig gamma 2b chain
692	78.5	4.9	348	2	S03273	Ig alpha chain C r	765	77	4.8	328	2	I47159	Ig gamma 2a chain
693	78.5	4.9	357	2	I36966	MHC class I protei	766	77	4.8	329	2	A44065	fibroblast growth
694	78.5	4.9	365	2	JH0535	class I histocompa	767	77	4.8	339	2	I56071	MHC class I histoc
695	78.5	4.9	365	2	I83063	Al1.2 - human	768	77	4.8	355	1	LKCH	proteoglycan link
696	78.5	4.9	366	2	I37527	MHC class I histoc	769	77	4.8	365	2	I37542	MHC class I histoc
697	78.5	4.9	368	2	T24408	hypothetical prote	770	77	4.8	366	2	I81232	lymphocyte antigen
698	78.5	4.9	393	1	GIW5M	Ig gamma-1 chain C	771	77	4.8	366	2	I37135	MHC class I histoc
699	78.5	4.9	403	2	I52590	m3-B isoform - mo	772	77	4.8	370	1	HLHUA3	MHC class I histoc
700	78.5	4.9	432	2	D83904	cabon storage regu	773	77	4.8	423	2	T23223	hypothetical prote
701	78.5	4.9	457	2	H85013	hypothetical prote	774	77	4.8	462	1	A37986	interleukin-6 rece
702	78.5	4.9	480	2	T04849	protein kinase hom	775	77	4.8	549	2	S04845	Ig heavy chain pre
703	78.5	4.9	545	2	JU0341	intercellular adhe	776	77	4.8	558	2	S68418	protein phosphatas
704	78.5	4.9	628	2	F84219	Htr16 transducer l	777	77	4.8	666	2	S01283	hypothetical prote
705	78.5	4.9	718	2	AF1620	hypothetical prote	778	77	4.8	790	1	TVHUTT	nerve growth facto
706	78.5	4.9	943	2	B45082	neurotrophic recep	779	77	4.8	1298	2	A64157	hypothetical prote
707	78.5	4.9	1036	2	B69368	hypothetical prote	780	77	4.8	1819	2	T32008	hypothetical prote
708	78.5	4.9	1183	2	S63046	probable membrane	781	77	4.8	1848	2	A44140	cellulose-binding
709	78.5	4.9	1280	2	E95031	alkaline amylopull	782	76.5	4.8	113	1	KVMS17	Ig kappa chain V r
710	78.5	4.9	1734	2	A41101	phorbol ester-bind	783	76.5	4.8	237	2	I54294	MHC HLA-DR-beta su
711	78.5	4.9	1742	2	S24600	prolectin - fruit	784	76.5	4.8	246	2	A47712	myelin/oligodendro
712	78.5	4.9	1813	2	T19295	hypothetical prote	785	76.5	4.8	266	2	A42621	MHC class II histoc
713	78	4.9	218	2	S22131	sucrose synthase (786	76.5	4.8	281	2	H90853	probable major tai
714	78	4.9	237	2	C60497	H-2 class II histoc	787	76.5	4.8	363	2	S07113	class I histocompa
715	78	4.9	248	1	MPRT0	myelin P0 protein	788	76.5	4.8	365	2	I84432	MHC class I protei
716	78	4.9	256	2	T24711	hypothetical prote	789	76.5	4.8	365	2	JL0135	MHC class I histoc
717	78	4.9	296	2	I46021	Fc-gamma receptor	790	76.5	4.8	366	2	B37028	MHC class I histoc
718	78	4.9	316	2	C37028	MHC class I histoc	791	76.5	4.8	379	2	E96842	hypothetical prote
719	78	4.9	342	2	T33768	hypothetical prote	792	76.5	4.8	406	2	D90492	hypothetical prote
720	78	4.9	362	2	C40730	class I histocompa	793	76.5	4.8	612	2	S33506	protein-tyrosine k
721	78	4.9	365	2	I36961	MHC class I protei	794	76.5	4.8	625	2	D87793	protein C27A12.2 l
722	78	4.9	366	2	T27949	hypothetical prote	795	76.5	4.8	772	2	A49069	collapsin - chicke
723	78	4.9	366	2	I37544	MHC class I histoc	796	76.5	4.8	830	1	B44047	glycoprotein B pre
724	78	4.9	366	2	I37523	MHC class I histoc	797	76.5	4.8	830	2	T44186	probable glycoprot
725	78	4.9	403	2	B88633	protein F56B3.9 li	798	76.5	4.8	831	1	VGBB6S	glycoprotein B - h
726	78	4.9	440	2	JL0144	interleukin-6 rece	799	76.5	4.8	891	2	H38790	hypothetical prote
727	78	4.9	460	2	JL0145	interleukin-6 rece	800	76.5	4.8	1152	2	AC1347	probable peptidogl
728	78	4.9	468	2	A41518	transcription fact	801	76.5	4.8	1611	1	WMTMPV	183K protein - pep
729	78	4.9	537	2	A46611	myosin-binding pro	802	76.5	4.8	2871	2	A55624	fibrillin-1 precur
730	78	4.9	556	2	A44441	B-cell antigen Cpl	803	76.5	4.8	5188	2	B85547	probable RTX famil
731	78	4.9	611	2	AB1497	internalin protein	804	76	4.7	171	1	RWHD1	T-cell surface gly
732	78	4.9	621	2	JQ1685	anthranilate synth	805	76	4.7	265	2	B39797	MHC class II histoc
733	78	4.9	621	2	S27752	hypothetical prote	806	76	4.7	274	2	A47639	OX-2 membrane glyc
734	78	4.9	717	2	T29816	host cell factor 1	807	76	4.7	277	2	I47162	Ig gamma 4 chain c
735	78	4.9	782	2	T43277	hypothetical prote	808	76	4.7	326	1	WMV215	B15R protein precu
736	78	4.9	931	2	T33744	hypothetical prote	809	76	4.7	326	2	T37450	interleukin-1 beta
737	78	4.9	954	2	T08961	hypothetical prote	810	76	4.7	349	2	JC6311	interferon recepto
738	78	4.9	954	2	E86174	protein F19P19.26	811	76	4.7	359	1	HLHU12	MHC class I histoc
739	78	4.9	1267	1	MXRX32	lambda 3 protein -	812	76	4.7	400	2	AD2260	hypothetical prote
740	77.5	4.8	160	2	I47163	cytolytic trigger	813	76	4.7	406	2	A35360	flagellar hook pro
741	77.5	4.8	229	1	TRBOTR	trypsin (EC 3.4.21	814	76	4.7	462	2	F83510	conserved hypotet
742	77.5	4.8	235	2	I68700	MHC HLA-A cell sur	815	76	4.7	476	2	A71302	conserved hypotet
743	77.5	4.8	238	2	I71907	MHC H2-IE-beta cel	816	76	4.7	477	2	S50738	QRIL protein - yea
744	77.5	4.8	264	2	S10989	class II histocomp	817	76	4.7	486	2	D64474	hypothetical prote
745	77.5	4.8	266	2	D39797	MHC class II histoc	818	76	4.7	498	2	S11246	LAG-3 protein prec
746	77.5	4.8	266	2	A25324	class II histocomp	819	76	4.7	521	2	I39956	neutral proteinase
747	77.5	4.8	266	2	I54448	MHC class II histoc	820	76	4.7	569	2	A36187	interleukin-1 rece
748	77.5	4.8	338	2	A39953	MHC class I histoc	821	76	4.7	569	2	A64642	T cell activation
749	77.5	4.8	339	2	A37028	MHC class I histoc	822	76	4.7	569	2	A97178	probable permease
750	77.5	4.8	365	2	JH0534	class I histocompa	823	76	4.7	856	2	I58411	protein-tyrosine k
751	77.5	4.8	365	2	I37477	MHC class I histoc	824	76	4.7	878	2	T08559	protein kinase hom
752	77.5	4.8	377	2	T05354	hypothetical prote	825	76	4.7	990	2	E90433	conserved hypotet
753	77.5	4.8	428	2	A82215	probable alanine r	826	76	4.7	1003	2	T13856	kar protein - frui
754	77.5	4.8	544	2	JC5018	intercellular adhe	827	76	4.7	1054	2	T30933	chitinase (EC 3.2.
755	77.5	4.8	573	2	T09940	calcium-dependent	828	76	4.7	1157	2	T40572	protein phosphatas
756	77.5	4.8	694	2	I40866	exo-alpha-sialidas	829	76	4.7	1177	2	T16594	hypothetical prote
757	77.5	4.8	1315	2	T28679	fibrinogen-binding	830	76	4.7	1267	1	MXRX31	lambda 3 protein -
758	77.5	4.8	1797	2	F69195	cell surface glyco	831	76	4.7	2185	1	JQ2021	genome polypeptide
759	77.5	4.8	2044	2	AB1180	probable peptidogl	832	76	4.7	2271	2	F90073	hypothetical prote

833	75.5	4.7	109	2	PH0091	Ig kappa chain V r	906	74.5	4.6	345	2	D97007
834	75.5	4.7	113	2	PL0203	anti-DNA autoantib	907	74.5	4.6	354	2	I34531
835	75.5	4.7	233	1	JU0284	Fc gamma (IgG) rec	908	74.5	4.6	354	2	I59308
836	75.5	4.7	238	2	A53278	MHC class II histo	909	74.5	4.6	354	2	I80166
837	75.5	4.7	251	2	I38053	myelin protein zer	910	74.5	4.6	354	2	I80167
838	75.5	4.7	266	2	I54295	lymphocyte antigen	911	74.5	4.6	354	2	I80165
839	75.5	4.7	340	2	S11143	class I histocompa	912	74.5	4.6	354	2	I80168
840	75.5	4.7	357	2	S18198	class I histocompa	913	74.5	4.6	362	2	I61861
841	75.5	4.7	358	2	S09268	Ig alpha chain C r	914	74.5	4.6	362	2	I37519
842	75.5	4.7	365	2	JH0536	class I histocompa	915	74.5	4.6	365	2	S16769
843	75.5	4.7	365	2	I37483	HLA-Aw34.2 antigen	916	74.5	4.6	365	2	JH0537
844	75.5	4.7	365	2	I38610	MHC class I histoc	917	74.5	4.6	365	2	I72170
845	75.5	4.7	366	2	JH0526	MHC class I histoc	918	74.5	4.6	365	2	I38436
846	75.5	4.7	393	2	C71254	hypothetical prote	919	74.5	4.6	365	2	I38519
847	75.5	4.7	412	2	B44418	surface antigen -	920	74.5	4.6	378	2	S61992
848	75.5	4.7	503	2	S63257	probable membrane	921	74.5	4.6	404	2	A46480
849	75.5	4.7	546	2	I48899	cortactin - mouse	922	74.5	4.6	409	1	G69000
850	75.5	4.7	566	2	C81870	probable single-st	923	74.5	4.6	432	1	RWQ974
851	75.5	4.7	610	2	AE1472	two-component sens	924	74.5	4.6	504	2	S00390
852	75.5	4.7	621	2	AC1974	hypothetical prote	925	74.5	4.6	524	2	A82580
853	75.5	4.7	646	1	S15901	chromogranin B pre	926	74.5	4.6	555	2	JQ1526
854	75.5	4.7	874	2	B86322	F6A14.8 protein -	927	74.5	4.6	575	2	T33881
855	75.5	4.7	891	2	T40137	hypothetical serin	928	74.5	4.6	578	2	T33880
856	75.5	4.7	1016	2	T00375	hypothetical prote	929	74.5	4.6	610	2	B84960
857	75.5	4.7	1133	1	EGRT	epidermal growth f	930	74.5	4.6	706	2	A81848
858	75.5	4.7	1289	2	F72308	hypothetical prote	931	74.5	4.6	766	2	S37894
859	75.5	4.7	4717	2	T41581	hypothetical coile	932	74.5	4.6	995	2	T27327
860	75	4.7	219	2	S38865	Ig kappa chain - m	933	74.5	4.6	1016	2	T19006
861	75	4.7	248	1	JH0252	myelin P0 protein	934	74.5	4.6	1052	2	T04439
862	75	4.7	306	2	T24589	hypothetical prote	935	74.5	4.6	1156	2	T23308
863	75	4.7	322	1	TVBYR2	GTP-binding protei	936	74.5	4.6	1507	2	T42631
864	75	4.7	322	2	A75067	abc transporter, p	937	74.5	4.6	1807	2	JC6319
865	75	4.7	326	2	H70782	probable ompA prot	938	74.5	4.6	3005	2	S33642
866	75	4.7	353	2	G02922	MHC class I Ler0-G	939	74	4.6	107	2	S57444
867	75	4.7	365	2	I37478	MHC class I histoc	940	74	4.6	121	2	S40371
868	75	4.7	366	2	I59622	lymphocyte antigen	941	74	4.6	135	2	P30563
869	75	4.7	398	2	I49443	gene 2B4 protein -	942	74	4.6	157	2	PH0201
870	75	4.7	474	1	OMH01B	alpha-1-B-glycopro	943	74	4.6	215	2	JB0242
871	75	4.7	507	1	A43387	polymerase-associ	944	74	4.6	259	2	A98049
872	75	4.7	507	2	S33192	phase-1 flagellin	945	74	4.6	259	2	F95181
873	75	4.7	507	2	JQ1929	phosphoprotein - r	946	74	4.6	263	1	HLMSBU
874	75	4.7	508	2	A53465	phase 1 flagellin	947	74	4.6	318	2	C81690
875	75	4.7	544	1	A48961	beta-amyase - Bac	948	74	4.6	344	2	A90040
876	75	4.7	551	2	G84301	hypothetical prote	949	74	4.6	359	2	I61867
877	75	4.7	620	2	AG1598	internalin like pr	950	74	4.6	368	2	A45831
878	75	4.7	648	2	T08898	envelope-like - so	951	74	4.6	438	1	HVRKC2
879	75	4.7	678	2	H82379	methyl-accepting c	952	74	4.6	447	2	T21716
880	75	4.7	748	2	I48744	semaphorin A - mou	953	74	4.6	455	2	AD1700
881	75	4.7	755	2	H86561	CT456 hypothetical	954	74	4.6	460	2	AE0656
882	75	4.7	755	2	S13288	hypothetical prote	955	74	4.6	476	2	A46118
883	75	4.7	854	2	S13288	env protein - huma	956	74	4.6	483	2	AH3445
884	75	4.7	875	2	H90371	proteinase [import	957	74	4.6	490	2	A35546
885	75	4.7	1055	2	AD2499	hypothetical prote	958	74	4.6	538	1	VGNZMM
886	75	4.7	1065	2	S19482	hypothetical prote	959	74	4.6	570	2	A57535
887	75	4.7	1104	2	S59310	probable membrane	960	74	4.6	573	2	A86253
888	75	4.7	1124	2	T30340	derRNA adenosine de	961	74	4.6	573	2	H96744
889	75	4.7	1176	2	A33856	surface-layer 125K	962	74	4.6	601	2	T11677
890	75	4.7	2175	1	GNNYBT	genome polypotein	963	74	4.6	604	2	S54032
891	75	4.7	2185	1	GNNYBT	genome polypotein	964	74	4.6	610	2	T22909
892	75	4.7	2193	2	S52919	polypotein (IA, 1	965	74	4.6	644	2	T20034
893	75	4.7	5105	2	T32650	hypothetical prote	966	74	4.6	754	2	S48020
894	74.5	4.6	112	1	KVWSS1	Ig kappa chain V r	967	74	4.6	855	2	A45713
895	74.5	4.6	112	2	F27887	Ig kappa chain V r	968	74	4.6	918	2	T02759
896	74.5	4.6	131	2	B39276	Ig light chain pre	969	74	4.6	1116	2	T31432
897	74.5	4.6	249	1	A61087	myelin P0 glycopro	970	74	4.6	1161	2	G81915
898	74.5	4.6	264	2	I48422	MHC class II histo	971	74	4.6	1217	2	F69823
899	74.5	4.6	266	2	B42621	MHC class II histo	972	74	4.6	1257	2	T09493
900	74.5	4.6	266	2	B39260	MHC class II histo	973	74	4.6	1445	2	T50508
901	74.5	4.6	321	2	D39371	Ig V-region-like B	974	74	4.6	1487	2	S15904
902	74.5	4.6	328	2	S30444	ST2 protein - huma	975	74	4.6	1827	2	T34288
903	74.5	4.6	344	2	B28967	T-cell surface gly	976	74	4.6	1975	2	B81192
904	74.5	4.6	345	2	E71600	rifin PFB1040w - m	977	74	4.6	1995	2	G81044
905	74.5	4.6	346	2	T33363	D-alanine-D-alanin	978	74	4.6	2013	2	A11489

hypothetical prote
histocompatibility
class I histocompa
class I histocompa
class I histocompa
class I histocompa
class I histocompa
MHC class I histoc
MHC class I histoc
MHC class I histoc
SLG1 protein - yea
Fc gamma (IgG) rec
polybdenum cofacto
T-cell surface gly
Ig gamma chain (cl
polyvinylalcohol d
interleukin-1 rece
hypothetical prote
hypothetical prote
GTP-binding protei
probable TonB-depe
hypothetical prote
hypothetical prote
ankyrin related pr
hypothetical prote
hypothetical prote
breast cancer tumo
integrin beta-4 ch
homeotic protein z
Ig kappa chain V-J
Ig kappa chain - h
T-cell receptor be
hypothetical prote
Ig kappa chain NTG
conserved hypothet
conserved hypothet
MHC class II histo
probable sodium-tr
hypothetical prote
MHC class I protei
MHC class I histoc
Ig mu chain C regi
hypothetical prote
UDP-N-acetylmuramo
hypothetical prote
hypothetical prote
GTP-binding protei
muscarinic acetyl
cell fusion glycop
intrleukin 1 recep
hypothetical prote
probable cytosolic
probable transcrip
probable amino aci
hypothetical prote
hypothetical prote
hypothetical prote
kinesin-related pr
Env transmembrane
hypothetical prote
K-Cl cotransport p
hypothetical prote
probable phosphoes
period protein hom
hypothetical prote
alpha-1 proteinase
hypothetical prote
hemagglutinin/hemo
hemagglutinin/hemo
probable peptidogl

979	74	4.6	3345	2	T13423	hypothetical prote	1052	73	4.5	449	2	E97428	chemotaxis motD pr
980	73.5	4.6	99	2	S24504	Ig kappa chain V r	1053	73	4.5	449	2	AF2646	chemotaxis MotD pr
981	73.5	4.6	109	2	PH0089	Ig kappa chain V r	1054	73	4.5	467	1	HLMSP3	poliovirus recepto
982	73.5	4.6	110	2	PH0090	Ig light chain V r	1055	73	4.5	479	2	S18447	variant surface gl
983	73.5	4.6	198	2	T19797	hypothetical prote	1056	73	4.5	504	2	A49467	occludin - chicken
984	73.5	4.6	223	2	T19793	hypothetical prote	1057	73	4.5	538	2	T19655	hypothetical prote
985	73.5	4.6	234	2	S14237	Ig kappa chain pre	1058	73	4.5	554	2	AE0584	asparagine synthet
986	73.5	4.6	237	2	F27060	class II histocomp	1059	73	4.5	568	1	S05532	gamma-glutamyltran
987	73.5	4.6	237	2	A42013	alpha-1-B-glycopro	1060	73	4.5	568	2	T05060	hypothetical prote
988	73.5	4.6	246	1	TRRT2	trypsin (EC 3.4.21	1061	73	4.5	771	2	T50299	hypothetical sarin
989	73.5	4.6	261	2	S29360	Fc gamma (IgG) rec	1062	73	4.5	793	2	AH1094	probable peptidogl
990	73.5	4.6	266	1	HLHUB	MHC class II histo	1063	73	4.5	848	2	C70203	DNA topoisomerase
991	73.5	4.6	266	1	B27618	MHC class II histo	1064	73	4.5	896	2	T47645	centromere protein
992	73.5	4.6	266	2	I54509	MHC class II HLA-D	1065	73	4.5	992	2	A39931	protein-tyrosine k
993	73.5	4.6	266	2	A39260	MHC class II histo	1066	73	4.5	1000	2	S18827	Flt3 protein - mou
994	73.5	4.6	297	2	D89404	hypothetical prote	1067	73	4.5	1048	2	T30815	platelet-derived g
995	73.5	4.6	318	2	D89742	hypothetical prote	1068	73	4.5	1090	2	C86450	PSD1.27 protein -
996	73.5	4.6	320	2	B86544	NADH (ubiquinone)	1069	73	4.5	1117	2	T19727	hypothetical prote
997	73.5	4.6	320	2	F27078	probable sodium-tr	1070	73	4.5	1167	2	A82543	chromosome segrega
998	73.5	4.6	354	2	S24440	class I histocompa	1071	73	4.5	1184	2	T09484	cartilage intermed
999	73.5	4.6	356	2	F71151	probable glucose-1	1072	73	4.5	1191	2	T31091	hypothetical prote
1000	73.5	4.6	362	2	C35997	MHC class I histoc	1073	73	4.5	1254	2	G86379	protein PSA9.24 [i
1001	73.5	4.6	362	2	I84488	lymphocyte antigen	1074	73	4.5	1341	2	T18301	latrophilin-2, spl
1002	73.5	4.6	362	2	I54505	lymphocyte antigen	1075	73	4.5	1354	2	T30884	latrophilin-2 (spl
1003	73.5	4.6	362	2	I54314	MHC HLA-B39N - hum	1076	73	4.5	1361	2	T30884	neural specific DN
1004	73.5	4.6	362	2	I59645	HLA-B-6701 - human	1077	73	4.5	1374	1	GNNVEC	genome polyprotein
1005	73.5	4.6	362	2	I68850	MHC class I histoc	1078	73	4.5	1407	2	T18381	latrophilin-2 (spl
1006	73.5	4.6	362	2	I61859	MHC HLA-B14 chain	1079	73	4.5	1420	2	T18385	latrophilin-2 (spl
1007	73.5	4.6	364	2	A35997	MHC class I histoc	1080	73	4.5	1820	2	A55494	latent transformin
1008	73.5	4.6	365	2	I84487	MHC HLA-A cell sur	1081	73	4.5	1856	2	C95008	immunoglobulin A1
1009	73.5	4.6	365	2	JH0544	class I histocompa	1082	73	4.5	1870	2	D88486	protein F20H11.2 [
1010	73.5	4.6	365	2	T37476	MHC class I histoc	1083	73	4.5	2143	2	G96595	hypothetical prote
1011	73.5	4.6	365	2	I37482	MHC class I histoc	1084	73	4.5	2960	2	A45259	desmoyokin - human
1012	73.5	4.6	366	2	I56034	gene HLA-C protein	1085	72.5	4.5	112	2	S38719	Ig light chain V r
1013	73.5	4.6	371	2	A88534	hypothetical 38.5K	1086	72.5	4.5	118	2	S24533	Ig kappa chain V r
1014	73.5	4.6	376	2	S70841	hypothetical trans	1087	72.5	4.5	118	2	S24507	Ig kappa chain V r
1015	73.5	4.6	394	2	T24860	hypothetical prote	1088	72.5	4.5	129	2	S40332	Ig kappa chain - h
1016	73.5	4.6	457	1	RMST4	T-cell surface gly	1089	72.5	4.5	131	2	S40372	Ig kappa chain V-J
1017	73.5	4.6	459	2	A6254	CD4 precursor - ra	1090	72.5	4.5	131	2	G32513	Ig kappa chain pre
1018	73.5	4.6	509	2	AD0649	probable secreted	1091	72.5	4.5	237	2	H28043	MHC class II histo
1019	73.5	4.6	553	2	A45987	polypeptide N-acet	1092	72.5	4.5	247	1	TRDG	trypsin (EC 3.4.21
1020	73.5	4.6	559	2	A49722	endoglin precursor	1093	72.5	4.5	247	2	S58394	myelin/oligodendro
1021	73.5	4.6	780	2	A48143	HF-1 regulatory el	1094	72.5	4.5	252	1	HLMSBF	H-2 class II histo
1022	73.5	4.6	820	2	D71471	probable DNA misa	1095	72.5	4.5	266	1	HLHUB	MHC class II histo
1023	73.5	4.6	890	2	T00800	disease resistance	1096	72.5	4.5	266	2	I56072	hypothetical prote
1024	73.5	4.6	979	2	B62207	hypothetical prote	1097	72.5	4.5	293	2	T31840	class I histocompa
1025	73.5	4.6	1042	2	A97209	spoID-like domain	1098	72.5	4.5	305	2	S07115	class I histocompa
1026	73.5	4.6	1066	2	T30297	dynein heavy chain	1099	72.5	4.5	308	2	I36956	MHC class II HLA-D
1027	73.5	4.6	1084	2	B64088	hemoglobin-binding	1100	72.5	4.5	343	1	S56493	probable alcohol d
1028	73.5	4.6	1188	2	T41696	probable C2-domain	1101	72.5	4.5	344	2	I49585	CD2 antigen protei
1029	73.5	4.6	1237	2	T08608	hypothetical prote	1102	72.5	4.5	353	2	B53250	class I histocompa
1030	73.5	4.6	1417	2	H90670	probable invasin [1103	72.5	4.5	354	2	S24433	class I histocompa
1031	73.5	4.6	1417	2	D85521	probable adhesin e	1104	72.5	4.5	354	2	I80170	class I histocompa
1032	73.5	4.6	4936	2	AH2515	hypothetical prote	1105	72.5	4.5	354	2	S24438	class I histocompa
1033	73	4.5	85	2	S08109	carcinoembryonic a	1106	72.5	4.5	358	2	S03538	class I histocompa
1034	73	4.5	231	2	S45089	hypothetical prote	1107	72.5	4.5	359	1	HLHUB4	MHC class I histoc
1035	73	4.5	234	2	S26453	hypothetical prote	1108	72.5	4.5	362	2	I36962	MHC class I protei
1036	73	4.5	247	2	A55717	myelin/oligodendro	1109	72.5	4.5	362	2	I56130	HLA-B*5401 - human
1037	73	4.5	278	1	T07TOX	OX-2 membrane gly	1110	72.5	4.5	362	2	I84486	transmembrane glyc
1038	73	4.5	294	2	S39606	class I histocompa	1111	72.5	4.5	362	2	I62042	MHC HLA-B cell sur
1039	73	4.5	333	1	HLHUB	T-cell surface gly	1112	72.5	4.5	362	2	I72755	HLA-B*5602 - human
1040	73	4.5	362	2	I62045	gene HLA B-1517 pr	1113	72.5	4.5	362	2	G01230	MHC class I histoc
1041	73	4.5	365	2	I38439	MHC class I histoc	1114	72.5	4.5	362	2	I59633	MHC HLA-B transmem
1042	73	4.5	365	2	I56039	HLA-A30.3 precuro	1115	72.5	4.5	362	2	I72753	HLA-B*5502 - human
1043	73	4.5	365	2	I61856	MHC class I histoc	1116	72.5	4.5	362	2	I59654	major histocompati
1044	73	4.5	365	2	I38518	HLA-A-0102 allele	1117	72.5	4.5	362	2	I72754	HLA-B*5601 - human
1045	73	4.5	366	2	I54430	MHC class I histoc	1118	72.5	4.5	362	2	I61863	MHC HLA-Bw46 - hum
1046	73	4.5	383	2	S29733	cysteine synthase	1119	72.5	4.5	362	2	I77966	MHC class I histoc
1047	73	4.5	390	2	T09000	cysteine synthase	1120	72.5	4.5	362	2	I72752	HLA-B*5501 - human
1048	73	4.5	401	2	C95986	probable dehydroge	1121	72.5	4.5	362	2	I61903	MHC class I histoc
1049	73	4.5	415	2	S00543	site-specific DNA-	1122	72.5	4.5	362	2	I62043	MHC HLA-B cell sur
1050	73	4.5	432	2	S30193	T-cell surface gly	1123	72.5	4.5	362	2	I37520	MHC class I histoc
1051	73	4.5	433	2	S26646	transcription fact	1124	72.5	4.5	362	2	I62041	MHC HLA-B cell sur

1125	4.5	362	2	I62044	MHC class I histoc	1198	4.5	756	2	C84682	hypothetical prote
1126	4.5	362	2	I61860	MHC HLA-B18 chain	1199	4.5	873	2	JC7079	homeobox protein 2
1127	4.5	362	2	I61789	class I histocompa	1200	4.5	901	2	JE0062	core protein VP3 -
1128	4.5	362	2	S25415	class I histocompa	1201	4.5	1188	2	T46608	zinc finger protei
1129	4.5	365	2	A45847	MHC class I histoc	1202	4.5	1389	2	T03273	embryogenesis tran
1130	4.5	366	2	I61866	MHC HLA-Cw2.2 cha	1203	4.5	1404	2	T19277	hypothetical prote
1131	4.5	369	1	T48720	translation initia	1204	4.5	1582	2	AC1153	adhesin homolog lm
1132	4.5	396	1	JH0631	cellular tumor ant	1205	4.5	1647	2	T49412	hypothetical prote
1133	4.5	432	1	RWC2T4	T-cell surface gly	1206	4.5	2256	2	AD1018	large repetitive p
1134	4.5	452	2	AG1339	hypothetical prote	1207	4.5	2364	2	I40884	cytotoxin L - Clos
1135	4.5	510	2	C84718	probable kinesin I	1208	4.5	4351	2	T00252	MEGF1 protein - ra
1136	4.5	609	2	T03476	conserved hypotet	1209	4.5	99	2	S24501	ig kappa chain v r
1137	4.5	649	2	D85135	hypothetical prote	1210	4.5	102	2	S14590	ig kappa chain v r
1138	4.5	682	2	H87407	3-phytase, fusion,	1211	4.5	103	2	PH1042	ig light chain v r
1139	4.5	686	2	T25987	hypothetical prote	1212	4.5	103	2	PH1043	ig light chain v r
1140	4.5	727	2	S54512	hypothetical prote	1213	4.5	110	2	S26335	ig kappa chain v r
1141	4.5	743	2	T15062	hypothetical prote	1214	4.5	114	2	A32987	ig kappa chain v r
1142	4.5	752	2	G90599	hypothetical prote	1215	4.5	118	2	S24536	ig kappa chain v r
1143	4.5	809	1	S43217	ubiquitin-protein	1216	4.5	118	2	S24503	ig kappa chain v r
1144	4.5	827	2	T20492	hypothetical prote	1217	4.5	118	2	S24535	ig kappa chain v r
1145	4.5	856	2	G70483	pyruvate, water di	1218	4.5	118	2	S24500	ig kappa chain v r
1146	4.5	859	2	S24571	env protein - huma	1219	4.5	118	2	S24532	ig kappa chain v r
1147	4.5	868	1	VCLJH4	env polyprotein -	1220	4.5	119	2	A49032	telokin - rabbit
1148	4.5	1034	2	S36758	mg11 protein - mou	1221	4.5	155	2	A41675	probable-ubiquitin
1149	4.5	1052	2	H83909	cell wall-associat	1222	4.5	157	2	S62571	sodium channel pro
1150	4.5	1084	2	T18292	nicotinamide nucle	1223	4.5	218	2	JC4788	class II histocomp
1151	4.5	1092	2	JX0312	differentiation-st	1224	4.5	220	2	A25925	MHC class II histo
1152	4.5	1299	2	A86366	T26J12.6 protein -	1225	4.5	247	2	JT0555	hypothetical prote
1153	4.5	1300	2	A36502	insulin receptor-r	1226	4.5	259	2	C85630	class II histocomp
1154	4.5	2287	2	T21312	hypothetical prote	1227	4.5	259	2	JC7109	ST2V protein - hum
1155	4.5	2356	2	T27790	hypothetical prote	1228	4.5	263	1	HLRTBB	class II histocomp
1156	4.5	3051	2	S42373	hypothetical prote	1229	4.5	266	1	HLHU3D	MHC class II histo
1157	4.5	3418	1	G02334	breast cancer tumo	1230	4.5	266	2	I54287	gene HLA-DRB1 prot
1158	4.5	3562	2	A47171	chondroitin sulfat	1231	4.5	266	2	A27618	class II histocomp
1159	4.5	114	2	PT0181	ig heavy chain v r	1232	4.5	279	2	S04693	T-cell receptor de
1160	4.5	115	1	K2HUCM	ig kappa chain V-I	1233	4.5	327	2	S39604	class I histocompa
1161	4.5	226	2	JC5327	adhesin complex 25	1234	4.5	335	2	A53434	cell surface glyco
1162	4.5	231	1	TRBQTR	trypsin (EC 3.4.21	1235	4.5	337	2	S31131	hypothetical prote
1163	4.5	235	2	S25058	ig kappa chain - m	1236	4.5	340	2	H88545	protein F59B2.11 (
1164	4.5	254	2	B72366	conserved hypotet	1237	4.5	347	2	H75427	S-layer-like array
1165	4.5	263	2	I62591	H-2 class II histo	1238	4.5	350	2	I50015	MHC class I protei
1166	4.5	290	2	F42527	B16R protein - vac	1239	4.5	354	2	S24436	class I histocompa
1167	4.5	296	2	T23380	hypothetical prote	1240	4.5	354	2	S24437	class I histocompa
1168	4.5	315	1	HNZVTV	hemagglutinin prec	1241	4.5	357	2	S11139	class I histocompa
1169	4.5	321	2	A42507	F5L protein - vacc	1242	4.5	361	2	I54418	MHC class I histoc
1170	4.5	321	2	T12497	hypothetical prote	1243	4.5	362	2	I37120	MHC class I histoc
1171	4.5	322	2	E36213	F5L protein - vacc	1244	4.5	362	2	B30345	MHC class I histoc
1172	4.5	351	2	C82755	conserved hypotet	1245	4.5	362	2	A45834	MHC class I histoc
1173	4.5	355	2	I80171	class I histocompa	1246	4.5	362	2	I61907	MHC class I histoc
1174	4.5	357	2	S12169	isopenicillin N ac	1247	4.5	362	2	I81233	lymphocyte antigen
1175	4.5	360	2	A27638	MHC class I histoc	1248	4.5	362	2	I37522	MHC class I histoc
1176	4.5	363	2	JH0542	class I histocompa	1249	4.5	362	2	I61904	MHC class I histoc
1177	4.5	363	2	S03537	class I histocompa	1250	4.5	362	2	I54457	MHC class I lympho
1178	4.5	366	1	HLHUW3	MHC class I histoc	1251	4.5	362	2	I56133	MHC class I protei
1179	4.5	366	2	JH0262	class I histocompa	1252	4.5	362	2	I84490	lymphocyte antigen
1180	4.5	370	2	AC1272	alanine dehydrogen	1253	4.5	362	2	I54238	gene HLA-B protein
1181	4.5	406	2	AH1822	geranylgeranyl hyd	1254	4.5	362	2	A30345	MHC class I histoc
1182	4.5	406	2	A10621	probable bacteriop	1255	4.5	362	2	A45880	MHC class I histoc
1183	4.5	434	2	T47748	alpha-galactosidias	1256	4.5	362	2	S24435	class I histocompa
1184	4.5	469	2	S61632	glycine hydroxymet	1257	4.5	362	2	S24434	class I histocompa
1185	4.5	541	2	T40745	probable histidine	1258	4.5	366	2	I38505	MHC class I histoc
1186	4.5	548	2	T25401	hypothetical prote	1259	4.5	393	2	JC6179	dorsal switch prot
1187	4.5	553	1	I46329	cell fusion glycop	1260	4.5	417	2	T01616	hypothetical prote
1188	4.5	553	1	VGNZND	cell fusion glycop	1261	4.5	442	2	D36718	dihydrolipoamide S
1189	4.5	565	2	I41061	flagellin - Escher	1262	4.5	470	2	S22080	ig heavy chain pre
1190	4.5	583	2	S29961	Ref(2)Pp protein -	1263	4.5	491	2	F81655	conserved hypotet
1191	4.5	590	2	S29964	ref(2)Pp protein -	1264	4.5	530	2	D70476	DNA helicase - Aqu
1192	4.5	594	2	T71661	penicillin-binding	1265	4.5	536	2	S71332	nauretic peptid
1193	4.5	595	2	B48658	flagellin - Escher	1266	4.5	547	1	A32244	60K cysteine-rich
1194	4.5	633	2	T19189	hypothetical prote	1267	4.5	566	2	G81151	single-stranded-DN
1195	4.5	643	2	T04847	probable serine/th	1268	4.5	583	2	T04327	phosphoglucosidase
1196	4.5	676	2	T47526	protein kinase-lik	1269	4.5	583	2	T04326	phosphoglucosidase
1197	4.5	711	2	C84767	hypothetical prote	1270	4.5	599	2	S06785	gene ref(2)P prote

1271	71.5	4.5	610	2	A11110	two-component sens	1344	71	4.4	879	2	A47704	endoglucanase I (E
1272	71.5	4.5	621	2	A71961	90kda chaperone -	1345	71	4.4	881	2	AE2153	DNA topoisomerase
1273	71.5	4.5	648	2	A85600	hypothetical prote	1346	71	4.4	961	2	T32493	unc-45 protein - C
1274	71.5	4.5	648	2	E90749	hypothetical prote	1347	71	4.4	1106	1	PFHUGB	platelet-derived g
1275	71.5	4.5	664	2	S59638	glucose transport	1348	71	4.4	1443	2	T31896	hypothetical prote
1276	71.5	4.5	664	2	S59637	glucose transport	1349	71	4.4	1526	2	T19473	hypothetical prote
1277	71.5	4.5	782	2	T27833	hoptry-associated	1350	71	4.4	1882	2	T00069	hypothetical prote
1278	71.5	4.5	830	1	A44047	glycoprotein B pre	1351	71	4.4	1946	2	AE1449	hypothetical prote
1279	71.5	4.5	858	2	A71392	RNA polymerase pro	1352	71	4.4	2139	2	A35672	crumbs protein - f
1280	71.5	4.5	862	2	AC1214	fibrinogen-binding	1353	71	4.4	2409	1	A60979	versican precursor
1281	71.5	4.5	876	2	T51951	gamma-adaptin 1 li	1354	71	4.4	4385	2	T29042	hypothetical prote
1282	71.5	4.5	888	2	A71720	hypothetical prote	1355	70.5	4.4	109	1	KVRT21	ig kappa chain v r
1283	71.5	4.5	901	1	P3XR17	core protein VP3 -	1356	70.5	4.4	112	2	S38716	ig light chain v r
1284	71.5	4.5	901	2	S07419	core protein P3 -	1357	70.5	4.4	112	2	A31807	ig kappa chain v r
1285	71.5	4.5	1008	2	T33672	hypothetical prote	1358	70.5	4.4	113	2	PL0205	anti-DNA autoantib
1286	71.5	4.5	1059	2	T22545	hypothetical prote	1359	70.5	4.4	113	2	B41940	ig light chain v r
1287	71.5	4.5	1186	2	AG1928	two-component hydr	1360	70.5	4.4	121	2	H27887	ig heavy chain v r
1288	71.5	4.5	1215	2	C84848	hypothetical prote	1361	70.5	4.4	128	1	GFHUC	glycophorin C - hu
1289	71.5	4.5	1270	2	S23464	viginin - chicken	1362	70.5	4.4	131	2	D34904	ig kappa chain pre
1290	71.5	4.5	1347	2	T30909	endo-1,4-beta-xyla	1363	70.5	4.4	144	2	B40098	colorectal cancer
1291	71.5	4.5	1539	2	S65775	homeotic protein H	1364	70.5	4.4	155	2	A26889	ig kappa chain (WM
1292	71.5	4.5	1576	2	T03277	pol protein - yeas	1365	70.5	4.4	197	2	S29593	ig kappa chain v r
1293	71.5	4.5	1608	2	A28182	hemolysin A - Serr	1366	70.5	4.4	218	2	S68241	ig kappa chain v r
1294	71.5	4.5	1834	1	JDW01	DNA-directed RNA p	1367	70.5	4.4	218	2	JCS810	monoclonal antibod
1295	71.5	4.5	1840	2	G85422	hypothetical prote	1368	70.5	4.4	237	2	C27060	class II histocomp
1296	71.5	4.5	2529	2	B64635	toxin-like outer m	1369	70.5	4.4	237	2	B28043	MHC class II histo
1297	71.5	4.5	2555	2	A40043	notch protein homo	1370	70.5	4.4	237	2	E28043	MHC class II histo
1298	71.5	4.5	2871	2	A55567	fibrillin I - bovi	1371	70.5	4.4	247	2	H83176	probable transcrip
1299	71	4.4	188	2	T41636	conserved hypothet	1372	70.5	4.4	250	2	A28564	lymphocyte functio
1300	71	4.4	225	2	S37484	ig kappa chain - m	1373	70.5	4.4	266	2	A39797	MHC class II histo
1301	71	4.4	251	2	A12647	flagellar biosynth	1374	70.5	4.4	288	2	A55737	membrane glycoprot
1302	71	4.4	251	2	H97429	flagellar biosynth	1375	70.5	4.4	303	2	A40807	probable RING fing
1303	71	4.4	260	2	I51542	MHC class II beta-	1376	70.5	4.4	306	2	A56344	copper homeostasis
1304	71	4.4	263	1	HLMSBK	H-2 class II histo	1377	70.5	4.4	307	2	S55596	hypothetical prote
1305	71	4.4	267	2	I56110	Fc-gamma RIIB-alp	1378	70.5	4.4	324	2	D64665	thioredoxin reduct
1306	71	4.4	272	2	S77576	oligopeptide trans	1379	70.5	4.4	327	1	G4HU	ig gamma-4 chain C
1307	71	4.4	274	2	S33440	T-cell receptor ga	1380	70.5	4.4	328	2	E64020	hypothetical prote
1308	71	4.4	311	2	JC7873	L-rhamnose-binding	1381	70.5	4.4	330	2	A29915	teratocarcinoma gl
1309	71	4.4	314	1	QXBP2L	hypothetical prote	1382	70.5	4.4	333	2	A96829	probable RING fing
1310	71	4.4	350	2	B43670	sulfate-binding pr	1383	70.5	4.4	348	2	A56247	natural killer cel
1311	71	4.4	353	2	I51572	maternal protein -	1384	70.5	4.4	352	2	A75098	glucose-1-phosphat
1312	71	4.4	355	2	I37516	HLA-B alpha-chain	1385	70.5	4.4	362	2	T38421	gene HLA B-1519 pr
1313	71	4.4	364	2	S03535	class I histocompa	1386	70.5	4.4	362	2	T51464	RING-H2 zinc fing
1314	71	4.4	365	2	S77963	MHC class I histoc	1387	70.5	4.4	380	2	B71122	hypothetical prote
1315	71	4.4	365	2	I54416	HLA-AW24 protein -	1388	70.5	4.4	406	2	A35401	cytochrome P450 10
1316	71	4.4	365	2	I54493	MHC class I histoc	1389	70.5	4.4	411	2	B70215	hypothetical prote
1317	71	4.4	366	2	I81231	lymphocyte antigen	1390	70.5	4.4	417	2	S76137	hypothetical prote
1318	71	4.4	366	2	I68712	MHC class I histoc	1391	70.5	4.4	430	2	T28143	tapasin I homolog,
1319	71	4.4	409	2	A48890	transcription acti	1392	70.5	4.4	466	2	JCS897	killer cell inhibi
1320	71	4.4	419	2	G72328	hypothetical prote	1393	70.5	4.4	515	2	F70786	probable pepA - My
1321	71	4.4	429	1	AJSCQG	phosphoribosylamin	1394	70.5	4.4	521	1	VGBEBB	glycoprotein gIII
1322	71	4.4	438	1	HVRKCS	ig mu chain C regi	1395	70.5	4.4	522	2	S60483	GDS1 protein - yea
1323	71	4.4	445	2	H71171	probable NADH oxid	1396	70.5	4.4	538	1	B60004	cell fusion glycop
1324	71	4.4	459	2	T04808	hypothetical prote	1397	70.5	4.4	559	2	A10135	DNA repair protein
1325	71	4.4	461	1	HVRK06	ig mu chain C regi	1398	70.5	4.4	564	2	AG2823	ABC transporter, m
1326	71	4.4	508	2	S54264	glycoprotein gC -	1399	70.5	4.4	564	2	F97601	afub (AE006182) [i
1327	71	4.4	514	2	S72443	DNA-binding protei	1400	70.5	4.4	583	2	T12574	phosphoglucomutase
1328	71	4.4	538	2	S52472	cell fusion protei	1401	70.5	4.4	585	2	S44851	K12H4.7 protein -
1329	71	4.4	540	1	OYHUCR	natruiretic peptid	1402	70.5	4.4	587	2	S41409	envelysin (EC 3.4.
1330	71	4.4	639	2	G88839	chitinase - Autogr	1403	70.5	4.4	593	2	H84779	hypothetical prote
1331	71	4.4	551	2	G72865	adhesin AP65-2 pre	1404	70.5	4.4	601	2	B36346	fibulin 1 precursor
1332	71	4.4	567	2	S69779	acetolactate synth	1405	70.5	4.4	603	2	T46236	hypothetical prote
1333	71	4.4	591	2	F64334	flagellin - Escher	1406	70.5	4.4	621	2	B64546	chaperone and heat
1334	71	4.4	595	2	A48658	myosin-binding C-p	1407	70.5	4.4	622	2	B44986	apical membrane an
1335	71	4.4	621	2	B57431	protein C10C6.5 (i	1408	70.5	4.4	648	1	G64826	probable ABC trans
1336	71	4.4	639	2	S88839	chitinase - Autogr	1409	70.5	4.4	683	2	C36346	fibulin 1 precursor
1337	71	4.4	690	2	S41009	hypothetical prote	1410	70.5	4.4	694	2	A83126	desmocollin 1b pre
1338	71	4.4	705	2	E88564	protein T05G5.9 (i	1411	70.5	4.4	770	2	B48910	probable MrCB peni
1339	71	4.4	710	2	E83360	conserved hypothet	1412	70.5	4.4	781	2	H95392	desmocollin la pre
1340	71	4.4	772	1	G89760	probable 5'-nucleo	1413	70.5	4.4	824	2	A48910	desmocollin la pre
1341	71	4.4	809	1	IJBODD	desmocollin 2a pre	1414	70.5	4.4	840	2	I37281	Dec1a precursor -
1342	71	4.4	863	1	IJBODC	hypothetical prote	1415	70.5	4.4	894	2	I37282	Dec1b precursor -
1343	71	4.4	867	2	T21311	S-layer protein pr	1416	70.5	4.4	983	2	A45583	receptor tyrosine

1417 70.5 4.4 1012 2 B97326
 1418 70.5 4.4 1035 2 FC1114
 1419 70.5 4.4 1237 2 A54080
 1420 70.5 4.4 1279 2 T13613
 1421 70.5 4.4 1331 2 T04938
 1422 70.5 4.4 1331 2 AE1843
 1423 70.5 4.4 1475 2 A42718
 1424 70.5 4.4 1483 2 C97012
 1425 70.5 4.4 1495 2 A85240
 1426 70.5 4.4 1495 2 T10649
 1427 70.5 4.4 1817 2 AD2165
 1428 70.5 4.4 2015 2 B81989
 1429 70.5 4.4 2149 2 C96695
 1430 70.5 4.4 2441 2 S39161
 1431 70.5 4.4 2459 2 AF2136
 1432 70.5 4.4 2468 2 A83412
 1433 70.5 4.4 2479 2 F87386
 1434 70.5 4.4 2616 2 A57096
 1435 70 4.4 127 2 S04574
 1436 70 4.4 162 2 I51668
 1437 70 4.4 188 2 AF1062
 1438 70 4.4 194 2 H97045
 1439 70 4.4 215 2 JE0244
 1440 70 4.4 232 1 HLMSE2
 1441 70 4.4 257 2 A71081
 1442 70 4.4 261 2 I52518
 1443 70 4.4 267 2 A35902
 1444 70 4.4 268 2 C71872
 1445 70 4.4 269 2 I51539
 1446 70 4.4 324 1 ZPBCS
 1447 70 4.4 324 2 H85908
 1448 70 4.4 358 2 AE2836
 1449 70 4.4 334 2 AH0300
 1450 70 4.4 340 2 B69446
 1451 70 4.4 347 2 S09274
 1452 70 4.4 358 2 AE2836
 1453 70 4.4 358 2 H97613
 1454 70 4.4 361 2 T34361
 1455 70 4.4 382 2 T33980
 1456 70 4.4 390 2 E81408
 1457 70 4.4 410 2 AB0735
 1458 70 4.4 411 2 S07472
 1459 70 4.4 412 2 S62538
 1460 70 4.4 441 2 D95124
 1461 70 4.4 473 2 B21159
 1462 70 4.4 479 1 BGBEF2
 1463 70 4.4 499 2 E84776
 1464 70 4.4 544 2 A47726
 1465 70 4.4 565 2 S29348
 1466 70 4.4 569 2 T23516
 1467 70 4.4 592 2 D88712
 1468 70 4.4 599 2 S29963
 1469 70 4.4 656 2 E71080
 1470 70 4.4 690 2 B82409
 1471 70 4.4 855 2 T10665
 1472 70 4.4 895 2 I54343
 1473 70 4.4 925 2 S50490
 1474 70 4.4 1014 2 T31109
 1475 70 4.4 1098 1 PFMSRB
 1476 70 4.4 1107 2 B91271
 1477 70 4.4 1107 2 B86112
 1478 70 4.4 1107 2 E65226
 1479 70 4.4 1178 2 S30431
 1480 70 4.4 1193 2 S68218
 1481 70 4.4 1212 2 T44236
 1482 70 4.4 1226 2 S44824
 1483 70 4.4 1232 2 T05322
 1484 70 4.4 1448 2 A12007
 1485 70 4.4 1690 2 T40847
 1486 70 4.4 1875 2 A36429
 1487 70 4.4 1919 2 T40032
 1488 70 4.4 2182 1 GNNYB1
 1489 70 4.4 2201 1 GNNYA9

endoglucanase fami
 SKDC25 protein -
 protein-tyrosine-p
 hypohetical prote
 hypohetical prote
 hypohetical prote
 nuclear pore compl
 probably celluloso
 hypohetical prote
 hypohetical prote
 two-component hybr
 hypohetical prote
 ribulose biphosph
 CREB-binding prote
 peptide synthetase
 hypohetical prote
 conserved hypohet
 nudel protein prec
 Ig kappa chain pre
 tumor suppressor -
 phase polarity sup
 hypohetical prote
 Ig kappa chain NIG
 H-2 class II histo
 hypohetical prote
 sperm acrosome ant
 Fc gamma (IgG) rec
 hypohetical prote
 MHC class II beta-
 signal peptidase I
 signal peptidase I
 signal peptidase I
 conserved hypohet
 hypohetical prote
 Ig alpha chain C r
 lytic murein trans
 hypohetical prote
 subillisin (EC 3.4
 probable periplasm
 conserved hypohet
 alpha-galactosidas
 hypohetical coile
 glycosyl transfera
 cell surface antig
 glycoprotein F - h
 hypohetical prote
 dis1-suppressing p
 glycine hydroxymet
 hypohetical prote
 protein C17H12.4 l
 Ref(2)Poz protein
 probable DNA-bind
 alpha-amylyase VCAO
 hypohetical prote
 dysroglycan - hum
 hypohetical prote
 myosin III - Atlan
 platelet-derived g
 probable periplasm
 hypohetical 123.8
 MSP-300 protein -
 botulinum neurotox
 f54f2.1 protein -
 hypohetical prote
 Subtilase family p
 probable rRNA biog
 integrin beta-4 ch
 hypohetical prote
 genome polyprotein
 genome polyprotein

1490 70 4.4 2228 2 B97942
 1491 70 4.4 2477 1 SUCHA
 1492 70 4.4 2664 2 T28626
 1493 70 4.4 3124 2 A40020
 1494 70 4.4 4135 2 T42629
 1495 69.5 4.3 92 2 S37502
 1496 69.5 4.3 102 2 S14591
 1497 69.5 4.3 102 2 S14594
 1498 69.5 4.3 107 2 S12954
 1499 69.5 4.3 111 2 S40359
 1500 69.5 4.3 111 2 PL0257

ALIGNMENTS

RESULT 1

S56749

functional adhesion molecule precursor - human

N;Alternate names: F11 platelet antigen; platelet adhesion molecule PAM-1; platelet F11

C;Species: Homo sapiens (man)

C;Date: 27-Oct-1995 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

C;Accession: A59406; S56749

R;Osaki, H.; Ishii, K.; Horiuchi, H.; Arai, H.; Kawamoto, T.; Okawa, K.; Iwamatsu, A.; K

J. Immunol. 163, 553-557, 1999

A;Title: Cutting edge: Combined treatment of TNF-alpha and IFN-gamma causes redistributi

A;Reference number: A59406; MUID:99323940; PMID:10395639

A;Accession: A59406

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-299 <OZA>

A;Cross-references: UNIPROT:Q9Y624; UNIPARC:UPI0000000DC1; GB:AAD42050; NID:G5326797; P

R;Naik, U.P.; Ehrlich, Y.H.; Kornecki, E.

Biochem. J. 310, 155-162, 1995

A;Title: Mechanisms of platelet activation by a stimulatory antibody: cross-linking of a

A;Reference number: S56749; MUID:95374438; PMID:7646439

A;Accession: S56749

A;Molecule type: protein

A;Residues: 28-49,'X',51-53,62-73,'E',75-103,123,'F',125-130,'PDKDXTIYLNKY','LT',206,'X'

A;Cross-references: UNIPARC:UPI00001468C7; UNIPARC:UPI00001468CD; UNIPARC:UPI00001468DI;

A;Note: the order of the peptides other than the amino terminus was not determined

C;Genetics:

A;Gene: JAM

C;Keywords: glycoprotein; phosphoprotein; platelet aggregation; platelet membrane

F;1-25/Domain: signal sequence #status Predicted <SIG>

F;26-299/Product: junctional adhesion molecule #status predicted <MAT>

Query Match 25.2%; Score 404; DB 2; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.9e-24;
 Matches 102; Conservative 46; Mismatches 126; Indels 16; Gaps 7;

Qy 2 ARSRHRLLLLLLYLV--VALGYHKAYGFSAPKDDQVVAVVEYQOEAILACKTPKKTVSS 59

Db 5 AQVERKLLCLFILAILLCSLALG-----SVTVHSSEPEVRIPENNPVKLSAYSGFS-SP 58

Qy 60 RLEWK-KLGRSVFVYQOTLQDGFKRAEMIDFNIRKNTVTRSDAGKYRCEVSAPSQG 118

Db 59 RVEWKFDQGGTTRLVYNNKITASYEDRVTLPTGTITFKSVTREDTGYTTCWVS--EBGG 116

Qy 119 QNLEEDTTLVLVAVAPVPSCEVPSSALSGTVVLRQDKEGNPAPEYTFKDGIRLLEN 178

Db 117 NSYGEVKVLIVLPSPKPTVNPSSATIGNRAVLVTSEQDGPSPSETFWFDGLVMTN 176

Qy 179 PRIGSQSTNSSYTMNTKTGTLOFNTVSKLDITGEYSCEARNISGVYRRCPGK-RMQVDDLNI 237

Db 177 PKSTRAFSNSSVYLNPTTGTGELVFDPLSLASDTGEYSCEARNISGVYRRCPGK-RMQVDDLNI 236

Qy 238 SGIIAAVVVALVISVGLGVCAQRKYGYSKETSFOKSSSSSKATTMSE 287

Db 237 GVIVAAVLVTLIGLILVFGIWFAYSRGHFDPR----TKKGTSSKKVIYSQ 282

RESULT 2

JC7780
cox sackie- and adenovirus receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 09-Jul-2004
C:Accession: JC7780
R:Hoelen, I.; Keyaerts, E.; Lindberg, M.; Van Ranst, M.
Biochem. Biophys. Res. Commun. 288, 805-808, 2001
A:Title: Characterization of a cDNA encoding the bovine coxsackie and adenovirus receptor
A:Reference number: JC7780
A:Contents: Liver
A:Accession: JC7780
A:Molecule type: mRNA
A:Residues: 1-365 <THO>
A:CROSS-references: UNIPROT:Q8MMV3; UNIPARC:UPI00000889CD; GB:AY033651
C:Comment: This protein serves as the primary adenoviral attachment site on bovine cells

Query Match 12.9%; Score 206.5; DB 2; Length 365;
Best Local Similarity 24.3%; Pred. No. 9.3e-09;
Matches 80; Conservative 49; Mismatches 135; Indels 65; Gaps 11;

QY 12 LLLRLVVALGVHRYKAYGFSAPKDDQVAVVEQEAAILACK---TPKKTVSSRLWE---- 63
DB 3 LLLRPLLCGVADFTRLGSLITTPQMIKAKETAYLFCCKFTLGPEDQGLDIEWLLSPA 62
QY 64 --KKL-----GRSVFVYVYQOTLQGFKNRAEMI-----DFNIRIKNVTRSDAGK 106
DB 63 DNQKVDQVILYSGDKIYDDYQ-----DLKGRVHFTSNDLKS GDASINVTNLQSLDGT 117
QY 107 YRCEV-SAPSSQOGNLEEDVTLEVLVAPVSPCEVPSALSGTVELRCQDKGKNPAPE 165
DB 118 YQCKVKAPGVGNKKIQ-----LTVLVKPSGIRCYVDGSEETGNDFKLCEPKGSLPLR 172
QY 166 YTFKDGIRLLENPLRGQSSTNSSTYMTKTKTGLQFNVTSKLDTGEYSCEARNVGYRRC 225
DB 173 YEWQK-----LSDSQKLTSMPLPMTSPVISVKNNAEYSGTYTCTVNRNVGSDQC 223
QY 226 -----PGKRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAKRGYFSKETSQFQ--- 274
DB 224 LLRLDVPVPSNRAGTIAGAVIGTLLALVLIIVFCCH-----KKREBEKEVEVHDI RE 279
QY 275 -----KNSSSKATMTSENVOMLTVPVIA 298
DB 280 DVPPPKSRTSTARSYIGSNHSLGSMSPS 308

RESULT 3
A41054
fasciclin II, transmembrane splice form precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 09-Jul-2004
C:Accession: A41054
R:Grenningloh, G.; Rehm, E.J.; Goodman, C.S.
Cell 67, 45-57, 1991
A:Title: Genetic analysis of growth cone guidance in Drosophila: fasciclin II functions
A:Reference number: A41054; MUID:92005695; PMID:1913818
A:Accession: A41054
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-811 <GRE>
A:CROSS-references: UNIPROT:P34082; UNIPARC:UPI000002A963; GB:M77165; NID:gi57402; PID:92005695
A:Gene: FlyBase:Fas2
A:CROSS-references: FlyBase:FBgn0000635
C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immunoglobulin-like domain
C:Keywords: membrane protein

Query Match 11.5%; Score 184; DB 2; Length 811;
Best Local Similarity 27.2%; Pred. No. 1.5e-06;
Matches 53; Conservative 37; Mismatches 75; Indels 30; Gaps 8;

QY 30 SAPKDDQVVAVVEQEAAILACKTPKKTVSSRLWEKKG---RSVSFVYVYQOTLQGFKNR 86
DB 142 NAPENQYPTLGQDY---VVMCEV-KADPNPIDLWRNGDPITNDKYVQVOT----- 189

RESULT 5
T29757
protein UNC-89 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-Dec-1999
C:Accession: T29757
R:Du, Z.; Le, T.T.; Wilson, R.
submitted to the EMBL Data Library, May 1997
A:Description: The sequence of C. elegans cosmid C09D1.
A:Reference number: Z20679
A:Accession: T29757
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6642 <DUZ>
A:CROSS-references: UNIPARC:UPI000017CF3C; EMBL:AF003131; PID: AAB54132.1; GSPDB:GN00019;
A:Experimental source: strain Bristol N2; clone C09D1
C:Genetics:

QY 87 AEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQOGNLEEDVTLEVLVAPVSPCEVPSAL 146
DB 190 -----NGLLRNVQESDEGIYTCR-AAVIETGELLER-TIRVEVFIQPEIISLPTNLEAV 242
QY 147 SGTVVVELRCQDKGKNPAPEYTWFKDGIRLLENPLRGQSSTNSSTYMTKTKTGLQFNVTSK 206
DB 243 ECKPFAANCTAR-GKPVPEISWIRDATQL-----NVATADRFQVNPQTGLVTISSVSQ 294
QY 207 LDTGEYSCEARNVSVG 221
DB 295 DDYGYTCLAKNRAG 309

RESULT 4
B41054
fasciclin II PI-linked splice form precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 17-Mar-2000
C:Accession: B41054
R:Grenningloh, G.; Rehm, E.J.; Goodman, C.S.
Cell 67, 45-57, 1991
A:Title: Genetic analysis of growth cone guidance in Drosophila: fasciclin II functions
A:Reference number: A41054; MUID:92005695; PMID:1913818
A:Accession: B41054
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-873 <GRE>
A:CROSS-references: UNIPARC:UPI0000177B17; GB:M77166
C:Genetics:
A:Gene: FlyBase:Fas2
A:CROSS-references: FlyBase:FBgn0000635
C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immunoglobulin-like domain
C:Keywords: transmembrane protein

Query Match 11.5%; Score 184; DB 2; Length 873;
Best Local Similarity 27.2%; Pred. No. 1.6e-06;
Matches 53; Conservative 37; Mismatches 75; Indels 30; Gaps 8;

QY 30 SAPKDDQVVAVVEQEAAILACKTPKKTVSSRLWEKKG---RSVSFVYVYQOTLQGFKNR 86
DB 142 NAPENQYPTLGQDY---VVMCEV-KADPNPIDLWRNGDPITNDKYVQVOT----- 189

QY 87 AEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQOGNLEEDVTLEVLVAPVSPCEVPSAL 146
DB 190 -----NGLLRNVQESDEGIYTCR-AAVIETGELLER-TIRVEVFIQPEIISLPTNLEAV 242
QY 147 SGTVVVELRCQDKGKNPAPEYTWFKDGIRLLENPLRGQSSTNSSTYMTKTKTGLQFNVTSK 206
DB 243 ECKPFAANCTAR-GKPVPEISWIRDATQL-----NVATADRFQVNPQTGLVTISSVSQ 294
QY 207 LDTGEYSCEARNVSVG 221
DB 295 DDYGYTCLAKNRAG 309

RESULT 5
T29757
protein UNC-89 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-Dec-1999
C:Accession: T29757
R:Du, Z.; Le, T.T.; Wilson, R.
submitted to the EMBL Data Library, May 1997
A:Description: The sequence of C. elegans cosmid C09D1.
A:Reference number: Z20679
A:Accession: T29757
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6642 <DUZ>
A:CROSS-references: UNIPARC:UPI000017CF3C; EMBL:AF003131; PID: AAB54132.1; GSPDB:GN00019;
A:Experimental source: strain Bristol N2; clone C09D1
C:Genetics:

A;Gene: CESP:unc-89

A;Map position: 1
A;Introns: 17/2; 108/3; 154/2; 211/2; 265/3; 326/2; 352/3; 426/2; 454/1; 500/1; 537/1; 673; 5917/1; 6027/1; 6061/3; 6153/2; 6515/1; 6552/3; 6609/1

Query Match 11.0%; Score 177; DB 2; Length 6642;
Best Local Similarity 28.8%; Pred. No. 6.7e-05;
Matches 62; Conservative 29; Mismatches 74; Indels 52; Gaps 11;

QY 28 GFAPKQDQVW---TAVEYQEAAILACKTPKKTSSRLWKKLGRSVSFVYQQTLOGDFK 84

DB 3823 GRAPFVELLSCTTVEQAILKCKV-XGEPRIKTKYKEKVEVEM-----SAR 3872

QY 85 NRAEMID---FNIRIKNTRSDAGKYRCVPSAPSEQONLEEDTVTLVLVAPVPSCEV 141

DB 3873 VRAEHKDDGTLTDFNVNQADAGEYRCB-AENYGSATWEGPIIVTLEGAPKIDG-EA 3929

QY 142 P-----SSALSGTVVELRCQDKEGNPAPEYTFWKDGIRLLENPLRGSQST 186

DB 3930 PDFLOPVKPAVTVGTAVLEGKI-----SGKPKPSVKWYKNGEELKPSDRVKIE-- 3979

QY 187 NSSYTMNTKTGLQFN-TVSKL-DTGEYSCEARNSVG 221

DB 3980 -----NLDDGTQRLTVTNKLLDDMDVEYCEASNEFG 4010

RESULT 6

I38346

elastic titin - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004

C;Accession: I38346

R;Label: S.; Kolmerer, B.

Science 270, 293-296, 1995

A;Title: titins: giant proteins in charge of muscle ultrastructure and elasticity.

A;Reference number: A57430; MUID:96026330; PMID:7569978

A;Accession: I38346

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-7962 <RES>

A;Cross-references: UNIPROT:Q10465; UNIPARC:UPI000011010C; EMBL:X90569; NID:g1017426; PID:g1017426

C;Genetics:

A;Gene: GDB:TN

A;Cross-references: GDB:127867; OMIM:186840

A;Map position: 2q31-2q31

Query Match 10.6%; Score 169.5; DB 2; Length 7962;

Best Local Similarity 28.6%; Pred. No. 0.00032;

Matches 55; Conservative 31; Mismatches 67; Indels 39; Gaps 7;

QY 40 AVEYQEAAILACKTPKKTSSRLWKKLGRSV-----SFVYQQTLOGDFKRAEMIDFN 93

DB 2661 SVEPKSIITLSTYTGTLPISTVTKKDGFNITTSKCNIVTTKTC-----I 2707

QY 94 IRKKNTRSDAGKYRCVPSAPSEQONLEEDTVTLVLVAPVPSCEV---PSSALSGT 149

DB 2708 LEINSTRKDAQYSCIEB--NEAGRDV-----CGALVSTLEPPYFVTELEPLEAAGD 2759

QY 150 VVELRCQDKEGNPAPEYTFWKDGIRLLENPLRGSQSTNSYTMNTKTGLQFNVTSLKDT 209

DB 2760 SVLSLQCC-VAGTPEITVSVWKDGLRPIPEYRTYFTNN-----VATLVFNKVNINDS 2811

QY 210 GEYSCEARNSVG 221

DB 2812 GEYTKCAENSIG 2823

RESULT 7

JE0100

neural cell adhesion molecule 2 - African clawed frog

N;Alternate names: N-CAM 2

C;Species: Xenopus laevis (African clawed frog)

C;Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004

C;Accession: JE0100

R;Kudo, M.; Takayama, E.; Tadakuma, T.; Shiokawa, K.

Biochem. Biophys. Res. Commun. 245, 127-132, 1998

A;Title: Molecular cloning of ssd-form neural cell adhesion molecules (N-CAMs) as the ma

A;Reference number: JE0099; MUID:98204770; PMID:9535795

A;Accession: JE0100

A;Molecule type: mRNA

A;Residues: 1-725 <KUD>

A;Cross-references: UNIPROT:O73634; UNIPARC:UPI00000FD757; DDBJ:AB008163; NID:g3116228;

A;Experimental source: heart

C;Comment: This protein mediates and regulates various cell-cell interactions through bo

C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu

F;413-475/Domain: immunoglobulin homology <IMM>

F;512-569/Domain: fibronectin type III repeat homology <3FR>

Query Match 10.1%; Score 162; DB 2; Length 725;

Best Local Similarity 27.1%; Pred. No. 7e-05;

Matches 56; Conservative 37; Mismatches 98; Indels 16; Gaps 8;

QY 29 FSAPKQDQVW---VTAVEYQEAAILACKTPKKTSSRLWKKLGRSVSFVYQQTLOGDFKNR 86

DB 300 YAKPKITTYVENKTAVELDEITLCEASGDPIPS-ITWRTAHRNIS--SEEXTLDGHIIVVK 356

QY 87 AEMIDFNIRIKNTRSDAGKYRCVPSAPSEQONLEEDTVTLVLVAPVPSCEVPSSAL 146

DB 357 DHIRMSALTLDKIQYTDAGEYFCVASNPFI-----GVDQMAMYFEVQYAPKIRG-PVWVVTW 411

QY 147 SGTVVELRCQDKEGNPAPEYTFWKDGIRLLENPLRGSQSTNSYTMNTKTGLQFNVTYSK 206

DB 412 EGNPVTITC-DVLAHPSAAVSWFRDG-OLLPS-----SNFSNIKIYNGFTFSLEVNPDSE 465

QY 207 LDTGEYSCEARNVGVRRCGPKRMQVD 233

DB 466 NDFGNTNCSAVNSIGHSESEFILLVQAD 492

RESULT 8

A41228

protein-tyrosine kinase (EC 2.7.1.112) Flk-1 precursor, endothelial cell-specific recept

C;Species: Mus musculus (house mouse)

C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 31-Dec-2004

C;Accession: A41228; I58365; S18832; S29991

R;Matthews, W.; Jordan, C.T.; Gavin, M.; Jenkins, N.A.; Copeland, N.G.; Lemischka, I.R.

Proc. Natl. Acad. Sci. U.S.A. 88, 9026-9030, 1991

A;Title: A receptor tyrosine kinase cDNA isolated from a population of enriched primitiv

A;Reference number: A41228; MUID:92020984; PMID:1717995

A;Accession: A41228

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1367 <MAT>

A;Cross-references: UNIPROT:P35918; UNIPARC:UPI0000028D93; GB:X59397; NID:g50976; PIDN:CA

R;Willauer, B.; Witzigmann-Voos, S.; Schumacher, H.; Martinez, R.; Moller, N.P.; Risau, W.;

Cell 72, 835-846, 1993

A;Title: High affinity VEGF binding and developmental expression suggest Flk-1 as a maj

A;Reference number: A46065; MUID:93208880; PMID:7681362

A;Accession: A46065

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-24,'T',26-782,'VL',785-916,'C',918-1367 <MIL>

A;Cross-references: UNIPARC:UPI000003CA97; GB:X70842; NID:g57923; PIDN:CAA50192.1; PID:g

A;Note: submitted to the EMBL Data Library, January 1993

A;Note: sequence extracted from NCBI backbone (NCBI:128064)

R;Oelrichs, R.B.; Reid, H.H.; Bernard, O.; Ziemlecki, A.; Wilks, A.F.

Oncogene 8, 11-18, 1993

A;Title: NYK/FLK-1: a putative receptor protein tyrosine kinase isolated from E10 embry

A;Reference number: I58365; MUID:93141255; PMID:8423988

A;Accession: I58365

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-678,'D',680-1340,'RSPV', <OEL>

A;Cross-references: UNIPARC:UPI0000170C47; GB:S53103; NID:g264004; PIDN:AAB25043.1; PID:g

C;Genetics:

A;Gene: FLK-1; NYK

C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; transmembrane
F:830-1165/Domain: protein kinase homology <KIN>
F:838-846/Region: protein kinase ATP-binding motif

Query Match 10.1%; Score 162; DB 2; Length 1367;
Best Local Similarity 24.7%; Pred. No. 0.00015;
Matches 55; Conservative 23; Mismatches 81; Indels 64; Gaps 7;

QY 35 QQVTVAVEQAEAILACKTPKTKVSRLEWKKLGRSVFVYQOTLQGFKNRAEMIDFN- 93
DB 554 QPAAPTEQESVSLTADRNTFEN-LTWYKLGQATSVHGESLTPCKNLDALWKLNG 612
QY 94 -----IRKNVTRSDAGKYRC-----EVSAPSEQQGNL 121
DB 613 TMSNSTNDIILVAFQNASLQDQGDYVCSAQDKTKRKHCLVQKLIILERNAPMITG-NL 671
QY 122 BEDTTLVLVAVAPVCEVPSSALSQGVTVLRQCKEGNPAPEYTFWKGIRLLENPRL 181
DB 672 ENQTTI-----GETIEVTC-PASGNPTPHITWPKDNETLVEDSGI 711
QY 182 GSQSTNSSTYNTKGTGLQFNVTSKLDTGEVSCSEARNVGVYRR 224
DB 712 VLRDGNRLITI-----RRVRKEDGGLYTCQACNVIGCAR 745

RESULT 9
A27681
non-specific cross-reacting antigen precursor - human
N:Alternate names: NCA; TEX/NCA
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1989 #sequence revision 16-Sep-1992 #text change 09-Jul-2004
C:Accession: A26902; A26875; A27681; B31037; A29918; A27709; A36271; C26414; E44476; F44
R:Oikawa, S.; Kosaki, G.; Nakazato, H.
Biochem. Biophys. Res. Commun. 146, 464-469, 1987
A:Title: Molecular cloning of a gene for a member of carcinoembryonic antigen (CEA) gene
A:Reference number: A26902; MUID:87298464; PMID:3619891
A:Accession: A26902
A:Molecule type: DNA
A:Residues: 1-141 <OIK>
A:Cross-references: UNIPROT:Q13774; UNIPARC:UPI0000072416; GB:M17082; NID:g180230; PIDN:
R:Thompson, J.A.; Pande, H.; Paxton, R.J.; Shively, L.; Padma, A.; Slimmer, R.L.; Todd, C
Proc. Natl. Acad. Sci. U.S.A. 84, 2965-2969, 1987
A:Title: Molecular cloning of a gene belonging to the carcinoembryonic antigen gene fami
A:Reference number: A29875; MUID:87204248; PMID:3033672
A:Accession: A29875
A:Molecule type: DNA
A:Residues: 23-141 <THO>
A:Cross-references: UNIPARC:UPI0000177070; GB:M16337
A:Note: the authors translated the codon ACT for residue 64 as Tyr
R:Tawaragi, Y.; Oikawa, S.; Matsuoaka, Y.; Kosaki, G.; Nakazato, H.
Biochem. Biophys. Res. Commun. 150, 89-96, 1988
A:Title: Primary structure of non-specific crossreacting antigen (NCA), a member of carc
A:Reference number: A27681; MUID:88106638; PMID:3337731
A:Accession: A27681
A:Molecule type: mRNA
A:Residues: 1-238, 'V', 240-344 <TAW>
A:Cross-references: UNIPARC:UPI000012748C; GB:M18728; NID:g189084; PIDN:AAA59907.1; PID:
R:Barnett, T.; Goebel, S.J.; Nothdurft, M.A.; Elting, J.J.
Genomics 3, 59-66, 1988
A:Title: Carcinoembryonic antigen family: characterization of cDNAs coding for NCA and C
A:Reference number: A31037; MUID:89122014; PMID:3220478
A:Accession: B31037
A:Molecule type: mRNA
A:Residues: 1-137, 'L', 139-344 <BAR>
A:Cross-references: UNIPARC:UPI000016ADC6; GB:M29541; NID:g189103; PIDN:AAA59915.1; PID:
A:Note: the authors translated the codon TTG for residue 138 as Phe
R:Neumaier, M.; Zimmermann, W.; Shively, L.; Hinoda, Y.; Riggs, A.D.; Shively, J.E.
J. Biol. Chem. 263, 3202-3207, 1988
A:Title: Characterization of a cDNA clone for the nonspecific cross-reacting antigen (NC
A:Reference number: A29918; MUID:88139389; PMID:2830274
A:Accession: A29918
A:Molecule type: mRNA
A:Residues: 1-344 <NEU>

A:Cross-references: UNIPARC:UPI000006DF42; GB:M18216; GB:J03550; NID:g178690; PIDN:AAAS1:
R:Grunert, F.; Kolbinger, F.; Schwarz, K.; Schwaibold, H.; von Kleist, S.
Biochem. Biophys. Res. Commun. 153, 1105-1115, 1988
A:Title: Protein analysis of NCA-50 shows identity to NCA cDNA deduced sequences and indi
A:Reference number: A27709; MUID:88268882; PMID:3390172
A:Accession: A27709
A:Molecule type: protein
A:Residues: 35-95; 99-120; 123-138; 149-151, 'X', 153-162; 166, 'X', 168-172, 'X', 174-193; 231-235;
078; UNIPARC:UPI0000177071; UNIPARC:UPI000017707C; UNIPARC:UPI000017707D;
R:Hefla, S.A.; Paxton, R.J.; Shively, J.E.
J. Biol. Chem. 265, 8618-8626, 1990
A:Title: Sequence and glycosylation site identity of two distinct glycoforms of nonspeci
A:Reference number: A36271; MUID:90256782; PMID:2341397
A:Accession: A36271
A:Molecule type: protein
A:Residues: 35-42; 44-53; 55-80; 83-134; 139-160; 166-172; 174-180; 191-194; 204-224; 233-308; 310;
082; UNIPARC:UPI0000177083; UNIPARC:UPI0000177084
R:Paxton, R.J.; Mooser, G.; Pande, H.; Lee, T.D.; Shively, J.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 920-924, 1987
A:Title: Sequence analysis of carcinoembryonic antigen: identification of glycosylation s
A:Reference number: A26414; MUID:87147209; PMID:3469650
A:Accession: C26414
A:Molecule type: protein
A:Residues: 35-69 <PAX>
R:Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstrom, S.
Genomics 14, 384-390, 1992
A:Title: Identification of three new genes and estimation of the size of the carcinoembry
A:Reference number: A44476; MUID:93052339; PMID:1427854
A:Accession: E44476
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 35-141 <KHA>
A:Cross-references: UNIPARC:UPI0000177086
A:Accession: F44476
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 35-137, 'L', 139-141 <KH2>
A:Cross-references: UNIPARC:UPI0000177086
C:Comment: This protein appears to be processed at the carboxyl terminus and anchored thr
C:Genetics:
A:Gene: GDB:NCA
A:Cross-references: GDB:120221; OMIM:163980
A:Map position: 19q13.2-19q13.2
A:introns: 22/1
A:Note: the list of introns may be incomplete
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termina
C:Keywords: blocked carboxyl end; glycoprotein; lipoprotein; membrane protein; phosphatic
F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-320/Product: nonspecific cross-reacting antigen #status experimental <MAT>
F:160-217/Domain: immunoglobulin homology <IMM1>
F:252-301/Domain: immunoglobulin homology <IMM2>
F:321-344/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:104,111,115,152,173,197,224,256,274,288,292/Binding site: carbohydrate (Asn) (covalent)
F:309/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:320/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Gly) (in mature form)

Query Match 10.0%; Score 161; DB 2; Length 344;
Best Local Similarity 26.5%; Pred. No. 3.4e-05;
Matches 58; Conservative 33; Mismatches 84; Indels 44; Gaps 10;

QY 41 VEYQAEAILACKTPKTKVSRLEWKKLGRSVFVYQOTLQGFKNRAEMIDFNIRKNVT 100
DB 157 VEDKDAVAFTCFQVNTTYLWVNV-GQSLVPSPRIQLSNG-----NMTITLSVK 206
QY 101 RSDAGKYCEVSAPEQQGNLBEDTTLVLVAVAPVCEVPSSA--LSGTVELRCQDK 158
DB 207 RNDAGSYECEIQNPASANRS---DPVTNLNVLPDGPFTIS-PSKANYRPGENLNLSC-H-A 261
QY 159 EGNPAPEYTFWKGIRLLENPRLGSGSTNSSTYNTKGTGLQFNVTSKLDTGEVSCSEARN 218

Db 204 LERNQRYIFLEPTQPLVFKTAFAPDPN--GKNI-KKEVGKILCTDCATPRLKMKMS 260
 QY 124 DVTTLVLVAPVAPVCEVPSSALSGTIVVELRCQDKEGNPAPETWFKDGIRLLENPRLS 183
 Db 261 QTGEV-----GEKSLKCEAAGNPQPSYRWFKDGKELNR-----S 296
 QY 184 QSTNSSYTMNTKTGTLOFNTVSKLDTGYSCEARNVSGYRRCPGKRMQVDDLNI-----S 238
 Db 297 RDIRIKYNGRKNRSLQFNKVKVEDAGEVCEANILGKDTVRG-RLHVNVSVTLLSSWS 355
 QY 239 GIIAAVVVVVALVISVGLGVGY 260
 Db 356 GHARKCNETAKSYCVNG-GVGY 376

RESULT 13
 THULIK
 leukocyte antigen-related protein precursor - human
 N:Alternate names: leukocyte common antigen homolog
 N:Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)
 C:Species: Homo sapiens (man)
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
 C:Accession: S03841; J00051
 J.Streuli, M.; Krueger, N.X.; Hall, L.R.; Schlossman, S.F.; Saito, H.
 J. Exp. Med. 168, 1523-1530, 1988
 A:Title: A new member of the immunoglobulin superfamily that has a cytoplasmic region ho
 A:Reference number: J00051; MUID:89035978; PMID:2972792
 A:Accession: S03841
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-1897 <SR>
 A:Cross-references: UNIPROT:P10586; UNIPARC:UPI0000132992; EMBL:Y00815; NID:G34266; PIDN
 C:Genetics:
 A:Gene: GDB:PTPRF; LAR
 A:Cross-references: GDB:120138; OMIM:179590
 A:Map position: lp34-1p34
 C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
 ogy

Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane
 F1-16/Domain: signal sequence #status predicted <SIG>
 F17-1897/Product: leukocyte antigen-related protein #status predicted <MAT>
 F17-1250/Domain: extracellular #status predicted <EXT>
 F17-99/Domain: immunoglobulin homology <IMM1>
 F139-199/Domain: immunoglobulin homology <IMM2>
 F236-290/Domain: immunoglobulin homology <IMM3>
 F308-390/Domain: fibronectin type III repeat homology <FN3A>
 F403-489/Domain: fibronectin type III repeat homology <FN3B>
 F501-583/Domain: fibronectin type III repeat homology <FN3C>
 F596-685/Domain: fibronectin type III repeat homology <FN3D>
 F698-798/Domain: fibronectin type III repeat homology #status atypical <FN3E>
 F810-893/Domain: fibronectin type III repeat homology <FN3F>
 F905-989/Domain: fibronectin type III repeat homology <FN3G>
 F1001-1078/Domain: fibronectin type III repeat homology <FN3H>
 F1251-1274/Domain: transmembrane #status predicted <TM>
 F1275-1897/Domain: intracellular #status predicted <INT>
 F1285-1897/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F1365-1586/Domain: protein-tyrosine-phosphatase homology <PTPI>
 F1654-1877/Domain: protein-tyrosine-phosphatase homology <PTP2>
 F44-97,146-197,243-288/Disulfide bonds: #status predicted
 F44-97,146-197,243-288/Disulfide bonds: #status predicted
 F107,240,285,711,956/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F1538/Active site: Cys (phosphocysteine intermediate) #status predicted
 F1544/Binding site: substrate phosphate (Arg) #status predicted
 F1829/Active site: Cys (phosphocysteine intermediate) #status predicted
 F1835/Binding site: substrate phosphate (Arg) #status predicted

Query Match 9.7%; Score 156; DB 1; Length 1897;
 Best Local Similarity 25.8%; Pred. No. 0.00066;
 Matches 59; Conservative 35; Mismatches 89; Indels 46; Gaps 10;

QY 11 LLLRLYLVALLGYHAYGFSAPKQDVVAVYQYQAILACKT---PKTVTSRLLEWKKG 67
 Db 8 LVNLGLVAGAGDSKPVFKVDEQ---TGLSGGVASFVCAATGEPK----PRTWKKKG 60

QY 68 RSVSVFYVYQOTLQDGFKNRAEMIDFN-----IRKNV-TRSDAGKYRCVVSAPSEOGQN 120
 Db 61 KKVS-----SORFEVIEFDGAGSVLRIOPLRVQRDEAIYECTATNSLGEINT 108
 QY 121 LEEDVTTLVLVAPVAPVSC-----VPSSALSGTIVVELRCQDKEGNPAPETWFKDGIR 174
 Db 109 SAKLSVLESEQLPPGPPSIDMGPKLVKVEKATATML---CA-AGNPDPDEISWFKDFLP 164
 QY 175 LLENPRLSQSTNSSYTMNTKTGTLOFNTVSKLDTGYSCEARNVSGYR 223
 Db 165 V-----DPAISNGRIKQLRSALQIESSESDQKYEVCVATNSAGTR 206

RESULT 14
 T23007
 hypothetical protein K09C8.5 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T23007; T23543
 R.Kershaw, J.
 submitted to the EMBL Data Library, November 1995
 A:Reference number: Z19651
 A:Accession: T23007
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-1328 <WIL>
 A:Cross-references: UNIPROT:O21043; UNIPARC:UPI00000823FD; EMBL:Z68005; PIDN:CAA91994.1;
 A:Experimental source: clone F59F3
 R.Kershaw, J.
 submitted to the EMBL Data Library, November 1995
 A:Reference number: Z19755
 A:Accession: T23543
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-1328 <W12>
 A:Cross-references: UNIPARC:UPI00000823FD; EMBL:Z68006; PIDN:CAA91999.1; GSPDB:GN00028;
 A:Experimental source: clone K09C8
 C:Genetics:
 A:Gene: CESP:K09C8.5
 A:Map position: X
 A:Introns: 34/1; 85/3; 133/3; 182/2; 220/3; 262/2; 390/3; 442/2; 493/3; 563/2; 586/3; 611/3

Query Match 9.7%; Score 155.5; DB 2; Length 1328;
 Best Local Similarity 27.5%; Pred. No. 0.00047;
 Matches 42; Conservative 34; Mismatches 66; Indels 11; Gaps 4;

QY 69 SVSVFYVYQOTLQDGFKNRAEMIDFNIRKNVTRSDAGKYRCVVSAPSEOGQNLEEDVTTL 128
 Db 382 TITLFEKQKLTESRKHKTNGSVLKIFFFLNTDIGYECVASNGEESKSHI--FSVSL 439
 QY 129 EVLVAPVAPVSCVPSSALSGTIVVELRCQDKEGNPAPETWFKDGIRLLENPRLSQSTNS 188
 Db 440 KESEQPVIIIDAPMDTNATIGQQVTLRCNAK-GFPVDPVVMVLFEGIRI---PR-----RNT 490
 QY 189 SYTMNTKTGTLOFNTVSKLDTGYSCEARNVSG 221
 Db 491 RYTISDNNIELTIEKVRHDSGVFTCOAVNSVG 523

RESULT 15
 T34416
 hypothetical protein F12F3.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T34416
 R.Fulton, B.; Wohldmann, P.
 submitted to the EMBL Data Library, July 1998
 A:Description: The sequence of C. elegans cosmid F12F3.
 A:Reference number: Z21521
 A:Accession: T34416
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-2783 <FUI>

A;Cross-references: UNIPARC:UPI00017B8E5; EMBL:U80022; PIDN:AAC25886.1; GSPDB:GN00023;
A;Experimental source: strain Bristol N2; clone F12F3
C;Genetics:
A;Gene: CESP:F12F3.2
A;Map position: 5
A;Introns: 45/3; 90/3; 451/3; 509/1; 2313/3; 2341/3; 2378/3; 2414/2; 2453/3; 2474/2; 252

Query Match 9.7%; Score 155.5; DB 2; Length 2783;
Best Local Similarity 30.4%; Pred. No. 0.0012;
Matches 58; Conservative 15; Mismatches 77; Indels 41; Gaps 6;

QY 86 RAEMIDENIRIKNVTESDAGKYRCEVSAPSEQONLEEDTTLVLVAPVP----- 137
Db 2606 RNEGDKFILRIANVTADAGKYELTAINPSGQANAELELTVVOSTTKTVGAKPKFNESPI 2665

QY 138 --SCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRL---LENPRLGSSQSTNSSYTM 192
Db 2666 VQTCENRAELRASP-----SGTPACRWFYNGNELIDGLDGYTTTSSDTNSS--- 2714

QY 193 NTKTGLQNTVSKLDTGYSCEARNVSVYR-----RCPGKRMQVDDLNISGIIA 242
Db 2715 -----LLINSVDKKHFGYLCYLTIRNQNGEELANAMILSEGC-RKHPRIDIYFVCNSFI 2767

QY 243 AVVVVALVISV 253
Db 2768 FSVVHLLISI 2778

Search completed: April 10, 2007, 16:34:37
Job time : 69 secs